sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:* sp_organelle:* sp_plant:* sp_rodent:* SPTREMBL_19:* sb_phage: * Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*
sp_unclassified:*

sp_virus:*

sp_bacteriap:*

sp_rvirus:*

sp_archeap:*

SUMMARIES

	Description	083001-060040	SOSSI SCIEDIOCOCC	Offold nontoction	Carata percoartept	DOOD THE CIECA	Observation arabidopsis	Casella streptococc	Uyskpu arabidopsis	096246 arabidopsis	Qystyb staphylococ	Q91255 petromyzon	09s4k2 lactobacill	O9wza6 thermotoga	09u459 plasmodium	053837 calmonolla	BITOMETE COCCE	Osuege manduca sex	. Objyk4 neisseria m
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395 KPEE 398
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        NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300
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                                                                                                                                                                                                                                                                                        Kastern W., Holst E., Nielsen E., Sjobring U., Bjorck L.;
"Protein L, a bacterial immunoglobulin-binding protein and possible
virulence determinant.";
                                EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptostreptococcus magnus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostriddaceae;
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"Structure of peptostreptococcal protein L and identification of repeated immunoglobulin light chain-binding domain.";
J. Biol. Chem. 267:12820-12825(1992).
EMBL, M86697; AAA2512.1;
InterPro; IPR003147; Bl.
InterPro; IPR001899; Gram_pos_anchor.
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719 PROTEIN L.
78983 MW; 963ABD76D5E34DD2 CRC64;
                                                                                                                                                                                            Last sequence update)
Last annotation update)
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llarity 100.0%; Pred. No. 2.5e-78;
Conservative 0; Mismatches 0;
                                                                                                                                                                                    Created)
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Pfam; PF00746; Gram_pos_anchor; 1.
                                                                                                                                                                                                                                                                                 MEDLINE-90215984; PubMed-2108927;
                                                                                                                                                                                                                                                                                                                  Infect. Immun. 58:1217-1222(1990)
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92316971; PubMed=1618782;
                                                                                                                                                                                PRELIMINARY;
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EKPEE 326
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Best Local Simi
Matches 304;
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Q51912;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murphy J.P., Trowern A.R., Duggleby C.J.;
"Nucleotide sequence of the gene for peptostreptococcal protein L.";
DNA Seq. 4:259-265(1994).
EMBL: L04466; AAA67503.1; -.
HSSP; Q51911; 1GAB.
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                                                                      LIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDE
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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25 992 PROTEIN L.
992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;
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Last annotation update)
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Interpro; IPR002988; GA.
Interpro; IPR01899; Gram_pos_anchor.
Pfam; PF0246; BB; 4.
Pfam; PF01468; GA; 4.
Pfam; PF0746; Gram_pos_anchor; 1.
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MEDLINE=95078460; PubMed=7987012;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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October 29, 2002, 09:25:41; Search time 29.364 Seconds (without alignments) 2556.865 Million cell updates/sec
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1 AVENKEETPETPETDSEEEV......GVDGVWIYDDAIKTFTVTEM 434
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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8: pp_organelle:*
9: sp_organelle:*
10: sp_plage:*
11: sp_rodent:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_artrus:*
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acore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_humān:* sp_invertebrate:* sp_mammal:* sp_mhc:*

	Description		_	O53975 streptococo	Q93em8 streptococc	Q54181 streptococc	Q56212 streptococc	Q53974 streptococc	Q53337 streptococc	Q9u8g8 manduca sex	Q91f88 arabidopsis	Q9aer7 staphylococ	Q9skp0 arabidopsis	Q9s4k2 lactobacill	Q93ty6 staphylococ	Q96246 arabidopsis
SUMMARIES	ID	053291	051912	053975	093EM8	054181	056212	053974	053337	0908G8	Q9LF88	Q9AER7	Q9SKP0	Q9S4K2	Q93TY6	096246
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	% Query Match	100.0	71.0	31.6	31.2	30.0	21.5	18.1	13.2	8.2	8.1	7.9	7.8	7.6	7.6	7.5
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"Nucleotide sequence of the gene for peptostreptococcal protein L.";
DNA Seq. 4.259-265(1994).
EMBL: L04466, AA67503.1; -.
HSSP: Q51911; 1GAB.
InterPro: IPR003147; B1.
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"Structure of peptostreptococcal protein L and identification repeated immunoglobulin light chain-binding domain.";
J. Biol. Chem. 267:12820-12825(1992).
EMBL. M86697; AAA25612.1;
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Kastern W., Holst E., Nielsen E., Sjobring U.,
"Protein L, a bacterial immunoglobulin-binding
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Pfam; PF00746; Gram_pos_anchor; 1.
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719 PRC
78983 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 76.3
Matches 334; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                          421 TYDDATKTFTVTEM 434
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SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR. C-TERMINAL IS SIMILAR TO OTHER STREPTOCOCCAL TYPE-III FC RECEPTORS.
                                    237
                                                              238 IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK 297
                                                                                                   321
                                                                                                                                       -----TTEAVDAATAEKVFKQYAND-----NGVDGEWTYDDATKTFTVTEK 364
                                                                                                                                                                                                                                                                                                                                                                                                      an
                                                                                                                                                                                            EPGEDTPEVQEGYATYE------EAEAAKEALKEDKVNNAYEVVQGADGRYYY 704
                                                                                                                                                                                                                                                                                                                   Streptococcus dysgalactiae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
298 K-----VDE----KPEEPM-----DTY-KLILNGKTLKG-----
                                                                                                                                                                                                                                                                                                                                                                                            Jonsson H., Mueller H.-P.;
"The type-III FC receptor from Streptococcus dysgalactiae is also alpha 2-macroglobulin receptor ";
Eur. J. Biochem. 220:819-826(1994).
                           AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT
                                                                                                                                                        599 HAGEETPELKDGYATYEEAEAAKEALKNDDVNNAYEIVQGADGRYYY--VLKIEVADEE
                                                                                                                                                                                                                                                                                                                                                                                                                                               PEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000724; IgG_bind_B.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF00778; IgG_bindingB: 5.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS000434; GRAM_POS_ANCHORING; UNKNOWN_1.
PROSITE; PS000430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal.
                                                                                                                                                                                                                                                                    EMBLrel. 01, Last sequence update)
EMBLrel. 17, Last annotation update)
BINDING PROTEIN MIG PRECURSOR (IGG BINDING
                                                                                                                                                                                                                                            664
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                                                                                                                                                                                                                                                             Created)
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IMMUNOGLOBIN G
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6 X 5 AA REPEATS OF [DEVP]-[DE]-[AT]-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                           IMMUNOGLOBIN G BINDING PROTEIN MIG.
                                                                                                                                                       EXTRACELLUÍAR (BY SIMILARITY).
MEMBRANE ANCHOR (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
2 X 24 AA REPEATS.
1-1.
                                                                                                                                                                                                                                                                                                                                                                  1-2.
5 X 70 AA TANDEM REPEATS
(IGG CONSTANT REGION-BINDING).
                                                                             ALPHA 2-MACROGLOBULIN-BINDING
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4A41CEEF7977862A CRC64;
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Last sequence update)
Last annotation update)
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51; Mismatches 14
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POTENTIAL
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Matches 192; Conserv
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SEQUENCE FROM N.A.
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Pfam; PF01378; IgG_binding_B; 3.
SEQUENCE 185 AA; 20118 MW; 114BAD7B500E3F62 CRC64;
                                                                                                                                                                                                                                                                              PRT;
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39.6%;
                                30.0%;
71.8%;
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                                                                                                                                                                                                     419 VWTYDDATKTFTVTE 433
                                                                                                                                                                                                                 171 VWTYDDATKTFTVTE 185
                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=25;
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=40041;
                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                     Matches 140;
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                                Query Match
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                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                           203 QAVQLEAPTVIDAPELTPALTTYKLVVKGNTF--SGETTTK----AIDTATAEKEFKQYA 256
                                                                                                                                                                                                                                                                    422
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Goward C.R., Murphy J.P., Atkinson T., Barstow D.A.;
"Expression and purification of a truncated recombinant streptococcal
                                                                                                                                                 51; Gaps
                                                                                                                                                                      24 ANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK-KDNGEYTVDVADKGYTL-.NIKFA- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus sp. 'group G'. Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
        MEDLINE=21437603; PubMed=11553540;
Song X.M., Perez-Casal J., Bolton A., Potter A.A.;
"Surface-Expressed Mig Protein Protects Streptococcus dysgalactiae
against Phagocytosis by Bovine Neutrophils.";
Infect. Immun. 69:6030-6037(2001).
                                                                                                                                                                                                                -----GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYA
                                                                                                                                                                                                                                                        126 DALKKDNGEYTVDVADKGYTLNIKFA - - - GKEKTPEEPKEEVTIKANLIYADGKTQTAEF
                                                                                                                                                                                                                                                                                                  183 KGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIK
                                                                                                                                                                                                                                                                                                               240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKV
                                                                                                                                                                                                                                                                                                                                                          300 DEKPE--EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATK
                                                                                                                                                                                                                                                                                                                                                                                               Length 669;
                                                                                                                                                 Indels
                                                                                   39 POTENTIAL.
669 MIG.
72682 MW; 5C8982B952029B03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                           Query Match 31.2%; Score 697.5; DB 2; Best Local Similarity 43.5%; Pred. No. 2.3e-26; Matches 190; Conservative 49; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein G.",
Blochem. J. 267:171-177(1990).
EMBL; X53324; CAA37410.1; -.
HSSP; P06654; 1PGX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 543 GVWTYDDATKTFTVTEM 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      418 GVWTYDDATKTFTVTEM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                  1
40
669 AA;
 STRAIN-ATCC 43078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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NCBI_TaxID=1320;
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                                                                                                                                                                                                                                                                                                                                                                                                            115 EEATA---EAYRYADALK---KDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 NLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKT 228
                                                                                                                                                                                                                                                     305 -----EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKT 358
                                                                                                                                                                                                                                                                                                               DASELTPAVTTYKLVINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKT 110
                                                                                                                                                                                                                                                                                                                                                                            FIVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDG 418
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                                                                                                                            247 GKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE-- 304
                                                                                                                                                                                         3 GETTTEAVDAATAEKVFKQY-----ANDNG------VDGEWTYDDATKTFTVTEKPEVI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CELL SURFACE PROTEIN PRECURSOR.
Streptococcus equi subsp. zooepidemicus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                               20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 481; DB 2; Length 429; Pred. No. 3.8e-16; 40; Mismatches 116; Indels
                                                            27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 CELL SURFACE PROTEIN.
44830 MW; 270D43F92C197BBA CRC64;
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SIGNAL 1 33 POTENTIAL.
Score 670; DB 2;
Pred. No. 1.1e-25;
3; Mismatches 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 AA
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"A protein G-related cell surface prote
zooepidamicus.";
Infect. Immun. 63:2668-2975(1995).
EMBL; U25852; AAA86832.1;
-. HSSP; P06654; IPCC.
InterPro; IPR001899; GA.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR000724; IgG_bind_B.
Pfam; PF01468; GA, I.
Pfam; PF01478; IgG_binding_B; 2.
Pfam; PF01478; IgG_binding_B; 2.
PRINTS; PR00015; GPOSANCHOR.
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13.2%;
96.6%;
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Best Local Similarity
Matches 56; Conserv
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                                                                                                         254 QIFRDYANKNGVDGVWAYDAATKIFTVTEQPVAETIEAAELIFPALTTYRLVIKGVTFSGE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANL-IYADGKTQTAEFKGTFEEATA 119.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 AQLKAYEDLAKLAADTDLDLDVAKIINDYTTKVENAKTAEDVK-----KIFEESQNEVT- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 KANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKK 298
141 DAASVDQVNAAIN----DAHTAIADITGA---ALLEAKEAAINELKQYGISDYYVTLINK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 AVVNAEESTVSPVTVATDAVT-------TSKEALAIINKLSEDN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus dysgalactiae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                 ----NIRFAGKKVDEKPEEP-MDTYKLILNGKTLKGETTTEAVDAATAE
                                                                                                                                                                                                            335 KVFKOYANDNGVDGEWTYDDATKTFTVTEKP--EVIDASELTPAVTTYKLVINGKTLKGE
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Jonsson H., Frykberg L., Rantamaeki L., Guss B.;

"Mac, a novel plasma protein receptor from Streptococcus ("ysgalactiae");

Gene 143:85-89(1994).

REMBI: 127798; AAA26921.1; -.

REMBI: 127798; AAA26921.1; -.

RESP: P06654; 1PGA.

RICEPTO: IPR001899; Gram_pos_anchor.

InterPro: IPR001899; Gram_pos_anchor.

Refam; PF01468; GA: 1.

Refam; PF01468; GA: 1.

Refam; PF00746; Gram_pos_anchor; 1.

Refam; PF00746; Gram_pos_anchor; 1.

Refam; PF00716; Gram_pos_anchor; 1.

Refam; PR00115; GRAM_POS_ANCHOR!

Refam; PR00115; GRAM_POS_ANCHOR!

Refam; PR00115; GRAM_POS_ANCHORING; UNKNOWN_1.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                               393 TTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTE 433
                                                                                                                                                                                                                                                                                                                                                                                       18.1%; Score 404; DB 2; L 32.3%; Pred. No. 1.9e-12; Live 31; Mismatches 110;
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
MAG PROTEIN PRECURSOR.
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                                                                 287 GYTI----
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                                                                                                                                                                299 VDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKT 358
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Sphingiodea; Sphingidae; Sphinginae; Manduca.

NCBI_TaxID=7130;
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MEDLINE-9377681; PubMed=8503988;

Cai S.Y., Wang Y.Y., Yao Z.J.;

"Structure analysis of streptococcal protein G Fc binding domain.";

Sci. China B 36:75-80(1993).

EMBL; S62801; AABZ7024.1;

HSSP; P06654: 1PGX.
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                                                                                                                              359 FTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDG
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Pfam; PF01378; IgG_binding_B; 1.
SEQUENCE 60 AA; 6655 MW; 924567E0D6B513DB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN G IGG FC BINDING DOMAIN.
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Pred. No. 4.2e-08;
1; Mismatches 1.
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EMBL; AF078161; AAF04457.1; -.
HSSP; P12111; ZKNT.
InterPro; IPR004094; Antistasin.
InterPro; IPR004598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
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Tormo M.A., Cucarella C., Amorena B., Lasa I., Penades J.R.;
The Bap Homolog Protein of Staphylococcus epidermidis RP62A Promotes
Biofilm Formation.";
Biofilm Formation.";
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EMBL, AY028618; AAK29746.1;
InterPro; IPR001298; Filamin.
InterPro; IPR001899; Gram_pos_anchor.
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   Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R., Welchselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 479;
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                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL132969; CAB86908.1; ...
InterPro; IRR004238; LEA.
Pfam; PF02987; LEA, 5.
SEQUENCE 479 AA: 52084 MW; C39E000D910E2385 CRC64;
                                                                     Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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24.1%; Pred. No. 0.11;
tive 59; Mismatches 195;
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Bacillus/Staphylococcus group; Staphylococcus
NCBI_TaxID=1282;
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Matches 110; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FBJ2_210.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viidiaplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 TYDDATKTFT---VTEKPEVID-ASELTPAVT--TYKLVINGKTLKGETTTKA---VDAE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 TPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKAT-SEAYAYADTLKKDNGEYTVDVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 KKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 ATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEE-----PKEEVTIKANLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 YADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 EEPMDTYKLILN-----GK-----TLKGETTTEAVDAATAEKVFKQYANDNGVDGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain; Serine protease inhibitor; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349364 MW; AB4ACD459C0D9134 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LATE EMBRYOGENESIS ABUNDANT PROTEIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 23.4%; Pred. No. 0.97;
Matches 106; Conservative 71; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.2%; Score 182.5; Di
3.4%; Pred. No. 0.97;
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                                                                                   Pfam; PF02822; Antistasin; 4.
Pfam; PF00047; ig; 2.
Pfam; PF00014; unitz_BPT1; 9.
Pfam; PF00014; unitz_BPT1; 9.
Pfam; PF00015; wap; 1.
PRINTS; PR00759; BASICPTASE.
SMART; SM00181; KU; 10.
SMART; SM00219; TSP1; 7.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 8.
PROSITE; PS500279; BPTI_KUNITZ_1; 10.
PROSITE; PS500279; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
InterPro; IPR002223; Kunitz_BPTI
                                                                  IPR002221; WAP
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SEQUENCE FROM N.A.
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RESULT 11 Q9LF88

Query Match

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EAAESTKEGAQIASEKAVGAK-----DATVEKAKET----ADYTAEKVGE 119
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                                                                                                                                                                                                                                                                                                                                                                                                        123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGTFEEATAE------AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAAT-----AEKV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NMEKAGEVTROKMEE-----MRLEGKELKEEAGAKAQEASOKTRESTESGAQKA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --FKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASEL------TPAVTTYKL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | : : | | | : : | | | | ETTRDSAAVRGNEAKGTIFGALGNVTEAIKSKLTMPSDIVEETRAAREHGGTGRTVVEVK 407
                                                                                                                                                                                                                                                                                                                                    63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DYAVDKA-----VEAKDKTAEKAKETANYTADKA-KEAKDKTAEK 204
                                                                                                                                                                                                                                                              3 ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae; Lactobacillus.
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"Genetic characterization of a cell envelope-associated proteinase from Lactobacillus helveticus CNRZ32.";
J. Bacteriol. 181.4592-4597(1999).
EMBL; AF133727; AAD50643.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 KLGELKDSAVETAKRAMGFLSGKTEEAKGKAVETKDT------AKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---EPKEEV--TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLED
                                                                                                                                                                                                                             Indels 142;
                                                                                                                                                                                            Length 448;
                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 VINGKTLKGETTTKAVDAETAEKAFKQYANDNG-VDGVWTYDDATK 427
                                                                                                                                                          C72563D4194DD9BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.8%; Score 175; DB 10;
24.5%; Pred. No. 0.23;
tive 50; Mismatches 160;
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                                                                                                                                                          48492 MW;
                                                                                      to the
                                                                                                    EMBL; AC006282; AAD20140.1;
InterPro; IPR004238; LEA.
Pfam; PF02987; LEA; 4.
SEQUENCE 448 AA; 48492 MW
                                                                                                                                                                                                           Best Local Similarity 24.5
Matches 114; Conservative
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 Nature 402:761-768(1999)
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                                                                                      (MAR-2000)
                                 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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MEROPS; S08.018; -.
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                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   966 PDGVTFDEAT-----TTTDESGNSETTFFI 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1009 EVKDTT----KPTVESVADQTQEVNTEIEPIKIEARDNSGQAVTNKVDGLPDGVTFDEATN 1065
                                                                                                                                                                                                                                                                                                 156
                                                                                                                                                                                                                                                                                                                                  847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPEEPMDTYKL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILNGKTLKGETTTEAVDAATAE----KVFKQYANDNG-----VDG---EWTYDDATK 357
                                                                                                                                                                                         672 TTEDTSIKGTAEVDTNINLTFNDGRTLNGKVDSNGNFSIA1PSYYVLTGKETIKITSIDK 731
                                                                                                                                                                                                                          GE----YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKG--- 112
                                                                                                                                                                                                                                                           GDNVSPAITISVIDK -- TPPAVKAISNKTOKVNTEIEPIKIEATDNSGQAVTNKVEGLPA 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                 PEEPKEEVTIKANLIYADGKTQTAEFKG----TFEEAT-----AEAYRYADLLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPETPETDSEEEVTIKANLIFANGSTQT - - AEFKGTFEKATSEAYAYA - - DTLK - - - KDN
                                                                                                                                                                                                                                                                                               113 --TFEEAT-----AEAYRYADALKKDNGE----YTVDVADKGYTLNIKFAGKEKT
                                                                                                                                                                                                                                                                                                                                790 GMTFDEATNTISGTPSEVGSYDITVTTTDENGNSETTTFTIDVEDT -- TKPTVESVADQT
                                                                                                                                                                                                                                                                                                                                                                                                    848 QEVNTEIEPIKIEATDNSGRAVTNKVDGLPDGVTFDEATNTISGTPSEVGSYDITVTTTD
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                                                                                                                       Indels 147;
                                                                                    Length 2402;
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|-----GLPDGV-TFDETTNTISGT 1159
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              PROSITE; PS50194; FILAMIN REPEAT; 2.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 2402 AA; 258095 WW; D5807D96BBF2E9CC CRC64;
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NY-2000 (TrEMBLrel. 13, Last sequence update)
NY-2001 (TrEMBLrel. 19, Last annotation update)
EMBRYOGENESIS ABUNDANT PROTEIN (ATECP63).
                                                                                    DB 2;
                                                                                                    Best Local Similarity 24.3%; Pred. No. 1.2; Matches 129; Conservative 49; Mismatches 205;
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                                                                                    Score 177.5;
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Pfam; PF00746; Gram_pos_anchor; 1.
                                                                                  7.98;
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01-MAY-2000 (
01-DEC-2001 (
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AT2G36640.
                                                                                    Match
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                                                                                                                                                                                                                                           1415 TLNL---DSENTVYTNKDKFTI-SGTISDDYKFYDLSINGNDVETSWSAVDYHSKEGIKK 1470
                                                                                                                                                                                                                                                                                          1756 VYTEKGHYFYKVVDRNAYRYRNYRNYGTKATLKRNSFVYQSNGKRASRKLLKKGTTITVYG 1815
                                                                                                                                                                                                                 73 TLNÍKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYADALKK 130
                                                                                                                                                                                                                                                                         131 DNGEYTVDVADKGYTLNIK------FAGKEKTPEEPKEE--VTIKANLIYA 173
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                               174 DGKTQTAEFK------GTFEEATAEAYRYADLLAKENGKYTVDVADKGY-----TL
                                                                                                                                                                                                                                                                                                                                                        1530 KATTDESEAKVVYSLDNGKTFNDVPADGFK ---- VTENGTVOFKAVDK -YGNESKVKSV
                                                                                                                                                                                                                                                                                                                                                                                      NIKFAGKEKTPEEPKEEVTIKANL---IYADGKTQ----TAEFKGTFAEATAEAYRYADL
                                                                                                                                                                                                                                                                                                                                                                                                                                             LAKENGKYTADLEDGGYTINIRFAGKKVDEKPEEPMDTYKLIL-NGKTLKGETTTEAVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 ATAEKVEKQYANDN-----GVDGEWTY-----DDATKTFT------VTEKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1696 AAPVHAEKDTKNDNKNTTEEGKDTKVMFKSVLYTKDLKKTRSTAQAYSSLKLVTEKGKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------EVIDASELTPA--VTTYKLVI------NGKTL-----KGETTTKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Bap, a Staphylococcus aureus Surface Protein Involved in Biofilm
                                                                                                                                                                                      125;
                                                                                                                                                          Length 1849;
                                                                                                                                                                                      Indels
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Penades J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 183:2888-2896(2001).
EMBL; AF288402; AAK38834.1; -.
SEQUENCE 2276 AA; 238792 MW; 8623C60472CB0C0F CRC64;
                                                                                                                              219F0D44B15A091F CRC64;
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Last annotation update)
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Bacteria: Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=1280;
                                                                                                                                                       7.6%; Score 170.5; DB 2; 25.9%; Pred. No. 1.9; attive 44; Mismatches 165;
                       * Pfam; PF02225; PA; 1.
Pfam; PF00082; Peptidase_S8; 3.
PRINTS; PR00082; SUBTILISIN.
PROSITE; PS00588; FLAGELLA_BB_ROD; UNKNOWN_1.
PROSITE; PS00136; SUBTILASE_HS9; 1.
PROSITE; PS00137; SUBTILASE_HS9; 1.
SEQUENCE 1849 AA; 199614 MM; 219F0D44B15?
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InterPro; IPR003137; PA.
InterPro; IPR000209; Peptidase_S8.
                                                                                                                                                                      Best Local Similarity 25.9% Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1879 TSEPSSA-----TSDATQ----VT 1909
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                                                                                                                                                                                                                        68 ADK-----GYTLNIKFAGKEKTPEEPK--------EEVTIKANLIYADGKTQT 107
                                                        Gaps
                                                                                                             8 TPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDV 67
                                                                                                                                                                                                                                                                          1599 PSNGDLNGGEELQVTATDKDGNTSEPSSANVTDTTASDAPTVNDVTSDATQVTGQAEPNS
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                                                        Indels 150;
7.6%; Score 170; DB 2; Length 2276; 21.8%; Pred. No. 2.6;
                                                        197;
                                                     47; Mismatches
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                                                        Conservative
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Matches 110; Conserv
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October 29, 2002, 09:25:41; Search time 20.636 Seconds (without alignments) 2556.865 Million cell updates/sec
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1565
1 AVENKEETPETPETDSEEEV......GGYTINIRFAGKKVDEKPEE 305
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
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3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:* sp_vertebrate:*
sp_unclassified:*
sp_rvirus:* sp_bacteriap:* sp_archeap:* sp_plant:*
sp_rodent:* sp_virus:* SPTREMBL_19:* 10: Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES		•
Result No.	Score	Query Match	Duery Match Length DB	DB	ID	Description	
-	1565	100.0	455	7	053291	Q53291 streptococc	
7	1561	99.7	719	~	Q51912	Q51912 peptostrept	
m	1226.5	78.4	992	~	051918	Q51918 peptostrept	
4	167	10.7	664	~	Q53975	Q53975 streptococc	
ι,	166	10.6	479	10	Q9LF88	Q91f88 arabidopsis	
9	166	10.6	699	7	Q93EM8	Q93em8 streptococc	
7	151	9.6	448	10	Q9SKP0	Q9skp0 arabidopsis	
80	149	9.5	448	10	096246	096246 arabidopsis	
6	148.5	9.5	2276	7	Q93TY6	Q93ty6 staphylococ	
, 10	141.5	9.0	1110	13	091255	Q91255 petromyzon	
11	141	9.0	1849	7	Q9S4K2	Q9s4k2 lactobacill	
12	137.5	8.8	992	16	Q9WZA6	Q9wza6 thermotoga	
13	137.5	8.8	5458	2	Q9U459	Q9u459 plasmodium	
,14	136	8.7	909	~	053837	Q53837 salmonella	
15	134.5	8.6	3198	Ŋ	Q9U8G8	Q9u8g8 manduca sex	
16	132.5	8.5	737	16	Q9JYK4	Q9jyk4 neisseria m	

0955ym2 procambarus 004111 enterococcu 086489 staphylococ 069188 streptococc 033742 streptococc 030874 streptococc 099446 streptococc 09922f7 staphylococ 09122f7 staphylococ 092774 listeria in P87344 theragra ch 092744 listeria in P87344 theragra ch 092745 streptococc 095745 streptococc 095745 streptococc 096765 streptococc 096765 streptococc	04.709 xenopus la 01309 xenopus la 021380 caenorhabdi 0940K5 streptcococc 045574 bacillus sp 05m955 arabidopsis 025920 plasamodium 039871 glycine max 091435 caenorhabdi 049547 mycoplasma 099948 staphylococ 053834 salmonella 096449 phytophthor
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132.5 131.5 131.5 130.5 130.5 130.5 130.5 128.5 128.5 127.5 127.5 127.5	12.7 126.5 126.5 125.5 125.5 125.5 125.1 125.1 124.5
L1112222222222222222222222222222222222	2 6 6 7 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9

ALIGNMENTS

	Q53291 PRELIMINARY; PRT; 455 AA.	01-NOV-1996 (TrEMBLrel. 01, Created)	(TrEMBLrel.	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	PROTEIN LG (FRAGMENT).	Streptococcus sp.	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;	Streptococcus.	NCBI_TaxID=1306;	[1]	SECUENCE FROM N.A. MEDI.INSE93094283: PubMed=1450053:	rn W., Bjorck L.;	"Protein LG: a hybrid molecule with unique immunoglobulin binding	properties.";	J. Biol. Chem. 267:25583-25588(1992).	EMBL; S50809; AAA03280.1;	HSSP; P06654; 1PGX.	InterPro; IPR003147; Bl.	InterPro; IPR000724; IgG_bind_B.	Pfam; PF02246; B1; 4.	Pfam; PF01378; IgG_binding_B; 2.		SEQUENCE 455 AA; 49926 MW; 381FC235BBC8307B CRC64;	.08)	Pred. No. 9.1e-79;	ches 305; Conservative 0; Mismatches 0; Indeis 0; Gaps	1 AVENKEETPETPETPSEEVTIKANLIFANGSTOTAEFKGTFEKATSEAYAYADTLKKDN 60			61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120	82 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 141
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395 KPEE 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90215984; PubMed-2108927;
Kastern W., Holst E., Nielsen E., Sjobring U., Bjorck L.;
"Protein L, a bacterial immunoglobulin-binding protein and possible
                                                                                                       AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA
                      EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptostreptococcus magnus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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MEDLINE-92316971; PubMed-1618782;
Bjoerck L., Sjoebring U., Kastern W.;
"Structure of peptostreptococcal protein L and identification of repeated immunosjobulin light chain-binding domain.";
J. Biol. Chem. 267:12820-12825(1992).
J. Biol. Chem. 267:12830-12825(1992).
InterPro; IPR001447; Bl.
InterPro; IPR001899; Gram_pos_anchor.
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Last annotation update)
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Matches 304; Conservative 0; Mismatches
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Pfam; PF00746; Gram_pos_anchor; 1.
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EKPEE 326
                                                                                                                                                                                                                                                       EKPEE 305
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299 EYTVDVADKGLTLAIKFAGKKEKPEEPKEEVTIKVALIFADGKTQTAEFKGTFEEATAKA 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murphy J.P., Trowern A.R., Duggleby C.J.;
"Nucleotide sequence of the gene for peptostreptococcal protein L.";
DNA Seq. 4:259-268(1994).
EMBL; L04466; AAA67503.1; -.
HSSP: Q51911; 1GAB.
275 FKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIFFHHHHHHHHHHHHHHH
                                                                                    238 IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
                                                                  LIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE.-KTPEEPKEEVTIKANLIYADGKTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptostreptococcus magnus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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25 992 PROTEIN L.
992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.4%; Score 1226.5; DB 2;
ilarity 79.9%; Pred. No. 8.5e-60;
Conservative 22; Mismatches 31;
                                                                                                                                                                                                                                                                                                          992 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR003147; B1.
Interpro; IPR002988; GA.
Interpro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02246; B1; 4.
Pfam; PF01468; GA; 4.
Pfam; PF00746; Gram_pos_anchor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=3316;
MEDLINE=95078460; PubMed=7987012;
                                                                                                                                                                                                                                                                                                   051918 PRELIMINARY;
051918;
01-NOV-1996 (TEMBLEEL: 01,
01-NOV-1996 (TEMBLEEL: 01,
01-DEC-2001 (TEMBLEEL: 19,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
--- SIMILARITY).
--- SIMILARITY:
TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR. C-TERMINAL IS SIMILAR TO OTHER STREPTOCOCCAL TYPE-III FC RECEPTORS.

EMBL; 229666; CAA874-1; ---
HSSP; P06654; 1PGX.
InterPro; IPRO01899; Gram_pos_anchor.
InterPro; IPRO00724; IGG_bind_B.
InterPro; IPRO00724; IGG_bind_B.
InterPro; IPRO00731; TonB_boxc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 X 5 AA REPEATS OF [DEVP]-[DE]-[AT]-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                Jonsson H., Mueller H.-P.; The type-III Fc receptor from Streptococcus dysgalactiae is also an
                                                                                                         Streptococcus dysgalactiae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IMMUNOGLOBIN G BINDING PROTEIN MIG PRECURSOR (IGG BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                              AFFINITY. N-TERMINUS MEDIATES BINDING TO PLASMA PROTEINASE INHIBITOR ALPHA 2-MACROGLOBULIN AFTER COMPLEX FORMATION WITH
                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMUNOGLOBIN G BINDING PROTEIN MIG
                                                                                                                                                                                                                                                            MEDILINE-99081771; PubMed-9864244;
Vasi J., Svensson J., Frick I.-M., Mueller H.-P.;
Vasi J., Svensson J., Frick I.-M., Mueller H.-P.;
Five homologous repeats of the protein G-related protein MIG
cooperate in binding to goat immunoglobulin G.";
Infect. Immun. 67.413.416(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pfam; PP00746; Gram_pos_anchor; 1.
Prfam; PP00746; Gram_pos_anchor; 1.
Prints Pr007015; GPOSANCHOR:
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
PROSITE; PS00430; TONB_DEPENDENT_RRC_1; UNKNOWN_1.
IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLUÍAR (BY SIMILARITY).
MEMBRANE ANCHOR (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 AA TANDEM REPEATS CONSTANT REGION-BINDING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHA 2-MACROGLOBULIN-BINDING
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4A41CEEF7977862A CRC64;
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                      664 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                           Created)
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1-1.
1-2.
5 x 7
(IGG (
                                                                                                                                                                                                                    alpha 2-macroglobulin receptor.";
Eur. J. Biochem. 220:819-826(1994)
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x ×
                                                                                                                                                                                    MEDLINE=94192673; PubMed=8143736;
                                                                                                                                                                SEQUENCE FROM N.A., AND FUNCTION
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                     PRELIMINARY;
                                           (TrEMBLrel.
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659
664
189
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639
660
87
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209
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349
419
489
592
630
                                                                                                                                 Streptococcus.
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                                          01-NOV-1996
                                                    01-NOV-1996
01-JUN-2001
                                                                                                                                                                          STRAIN-SC1
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TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                     FUNCTION
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REPEAT
DOMAIN
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DOMAIN
DOMAIN
                               053975;
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                     053975
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                                                                                     MIG).
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RESULT 4
          053975
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Length 664;

Decision of the control of the contr

10.7%; 27.4%;

Best Local Similarity

Query Match

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12;
     16;
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryotus, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                          -YADALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQT 179
                                                                                                                                                                                                                                                                         AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEV 236
                                                                                                                                                                                                                                                                                                                                                                         381 KAIDAATAEKEFKQYATANGV---DGEWSYDDATKTFTVTEKPAVIDAPELTPALTTYKL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEAT 118
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                                                                                                                                              VADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTAESTREGADIASEKAAGMR-----DTTGEVRDSTAOKTKETADYTADKAREAKD 125
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  40; Gaps
                                                  ETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVD 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAG
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; Pred. No. 0.062;
43; Mismatches 137; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.
Weichselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer:
Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project,
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL132969; CAB86908.1; -.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LATE EMBRYOGENESIS ABUNDANT PROTEIN-LIKE.
  Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 AA
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49;
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 25.8%
Matches 82; Conservative
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01-0CT-2000
84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          237
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SEQUENCE
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214 DAPELTPALTTYKLVVKGN-TFSGETTTKAIDTATAEKEFKQ-YATANNV---DGEWSYD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 VADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA-- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 DATKTFTVTEKPAVIDALELTPALTTYKLIVKGNTF--SGETTTK----AIDAATAEKEF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 YRYADALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 TAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 VTIKANLIYADGKTQTAEFKGTFAEATAEAYR-YADLLAKENGKYTADLEDGGYTINIRF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVD 66
                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus dysgalactiae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 43078;

BELLINE-1437603; PubMed=11553540;
Song X.M., Perez-Casal J., Bolton A., Potter A.A.;
"Surface-Expressed Mig Protein Protects Streptococcus dysgalactiae against Phagocytosis by Bovine Neutrophils.";
Infect. Immun. 69:6030-6037(2001).
EMBL; AF354651; AAL09476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 ELKDSAVDTAKRAMGFLSGKTEETKQKAVETKDTAKEKMDEAGEEARRKMEE-----
                                                         230 EEPKEEV-TIKANLIYADGKTQ-----TAEFKGTFAEATAEAYRYADLLAKENGKYTADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 669;
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Last annotation update)
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(TrEMBLrel. 13, Last seq
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72682 MW;
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------MRLEGKKLDE 355
                                                                                                                                           284 EDGGYTINIRFAGKKVDE 301
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nes 85; Conserv
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482 KTFTVTEKP 490
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                                                                                                                                                                                                                                                                                                                                                                                           MIG PRECURSOR
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01-MAY-2000
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Q9SKPO;
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SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
STRAIN=CV. COLUMBIA;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                      Arabidopsis thaliana (Mouse-ear cress). Eukaryophyta; Tracheophyta; Eukaryopty Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATECP63.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y-----KDYTVDKAKEAKDTTAEKAKETANYTADKA-VEAKDKTAEKIGEYK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 KGTFEEATAE-----AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update) LATE EMBRYOGENESIS ABUNDANT PROTEIN (ATECP63).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 AA; 48492 MW;
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02,
19,
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Matches 79; Conservative
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01-FEB-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
LEA PROTEIN IN GROUP 3.
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STRAIN-CV. COLUMBIA;
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1853 TIDIPSNVDLNGGEELQVTATDKDGNTSEPSSANVTDTTAPDAPTVNDVTSDATQVTGQA 1912
                                                                                                1685 PSNVDLNGGEELQVTATDKDGNTSEPSSANVTDTTAPDAPTVNDVTSDATQVTGQAEPNS 1744
                                                                                                                                                                                                                                                   1799 TNVTDTTASDAPTVNDVTSDASQVTGQAEPNST-VKLTFPDGTT-----ATGTADDQGNY 1852
                                   -----AD----DQGNYTIDI 1684
                                                                                                                                                                                                                  ------EEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKY 207
                                                                                                                                            108 AEFKGTFEEATAEAYRYADALKKDNGEYTVDVADK-----GYTLNIKFAGKEKTPEEPK- 161
                                                                        ---- EEVTIKANLIYADGKTQT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 NGEYTVDVADKGYT------LNIKFAGKEKTPEEPKEEVTIKANLIYADGKT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTAEFKGTFEEATAEA-----YRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEE--PKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADK 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFE-KATSEAYAVADTLKKD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAEKDEEEEEEEEEEKEEEE -----AEAEEEEEEDRGRKEGEAEAEEEEVEKEE
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   TPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petromyzon marinus (Sea lamprey).
Eukarvota; Metazoa; Chordata; Cranlata; Vertebrata; Hyperoartia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 1110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Jacobs A.J., Kamholz J., Selzer M.E.,
The single lamprey neurofilament subunit (NF-180) lacks
multiphosphorylation repeats and is expressed selectively in
projection neurons.",
E Brain Res. Mol. Brain Res. 29:43-52(1995).
R EMBL, U19361; AAA80106.1; -.
R InterPro; IPR00164; IF.
InterPro; IPR001633; Tropomyosin.
R Pfam; PF000184; Tropomyosin.
R PRINTS; PR00194; TROPOMYOSIN.
R PROSITE; PS001296; IF; UNKNOWN.1.
SEQUENCE 1110 AA; 123818 MW; 6558DA73DAF6974C CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   1913 EPNST-VKLTFPDGTT----ATGTADDQGNYTIDIPSNG 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%; Score 141.5; DB 13; 25.4%; Pred. No. 3.6; ative 38; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebra
Petromyzontiformes, Petromyzontidae, Petromyzon.
NCBL_raxID=7757,
                                                                                                                                                                                                                                                                                                                                                           248 KTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
                                 1644 TSDATQVTGQAEPNSTVKLTFPDGTTAT----GT---
                                                                        ADK -----GYTLNIKFAGKEKTPEEPK ------
                                                                                                                                                                                                                                                                                      TVDVADK - - - - GYTLNIKFAGKEKTPEEPK - -
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MEDLINE=95287814; PubMed=7770000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                              63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DYAVDKA------VEAKDKTAEKAKETSNYTADKA-KEAKDKTAEK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 KGTFEEATAE-----AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 VGEYKDYTVDKAVEARDYTAEKAIEAKDKTAEKTGEY-----KDYTVEKATEGKDVTVS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 KLGELKDSAVETAKRAMGFLSGKTEEAKGKAVETKDT------AKEN------MEK 302
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                      ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                            120 Y-----KDYTVDKAKEAKDTTAEKAKETANYTADKA-VEAKDKTAEKIGEYK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penades J.R.; "Bap, a Staphylococcus aureus Surface Protein Involved in Biofilm Formation.",
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                                                                STRAIN-COLUMBIA, TISSUE-DRY SEED;
MEDLINE-97169149; PubMed-9016956;
Yang H., Saitou T., Komeda Y., Harada H., Kamada H.;
"Arabidopsis thaliana ECP63 encoding a LEA protein is located chromosome 4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2276;
                                                                                                                                                                                                                                                                    DB 10; Length 448;
                                                                                                                                                                                                                                                                                   ; Pred. No. 0.49;
38; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cucarella C., Solano C., Valle J., Amorena B., Lasa I I.,
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EMBL; AF288402; AAK38834.1; -.
SEQUENCE 2276 AA; 238792 MW; 8623C60472CB0COF CRC64;
                                                                                                                                                                                                                                 DC37099F18FBA85E CRC64;
Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BIOFILM-ASSOCIATED SURFACE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.5%; Score 148.5; DB 2;
21.2%; Pred. No. 3.4;
ive 36; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2276 AA.
                                                                                                                                                                                                                                                                  9.5%; Score 149; 24.5%; Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGEVIROKMEEMRLEGKELKEE 324
                                                                                                                                                     Gene 184:83 48 (1997).
EMBL; D64140; BAA11017.1; -.
InterPro; IPR004238; LEA.
Pfam; PF02087; LEA. 4.
SEQUENCE 448 AA; 48534 MW;
                                                                                                                                                                                                                                                                                                     79; Conservative
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Best Local Similarity 21.2
Matches 72; Conservative
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                                                 SEQUENCE FROM N.A.
                NCBI_TaxID=3702
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Matches
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Q93TY6
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                                                                                         Thermotoga maritima
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                                                                                                                  NCBI_TaxID=2336;
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                                                                                                       Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 TLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYADALKK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNGEYTVDVADKGYTLNIK------FAGKEKTPEEPKEE--VTIKANLIYA 173
                                    ----VEAESKEEEEEDSKEADAEEDEAEEEEVKEEEVTKSDAEEAEAEAEEEAAKSEEE 739
                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                      MEDLINE-99350424; PubMed-10419958;
MEDLINE-99350424; PubMed-10419958;
Pederson J.A., Mileski G.J., Weimer B.C., Steele J.L.;
"Genetic characterization of a cell envelope-associated proteinase from Lactobacillus helveticus CNR232.";
Enceriol. 181:4592-4597(1999).
EMBL; ARI33727; AAD50643.1;
HSSP; P00782; ISUC.
          215 GYTLNIKFAGKEKTPEEPK------EEVTIKANLIYADGKTQTAEFKGTFAEATAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 DGKTQTAEFK------GTFEEATAEAYRYADLLAKENGKYTVDVADKGY-----TL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219F0D44B15A091F CRC64;
                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                     740 AAEEAKDEAEEEEAEEEAVEETEAATEEAEAKEASDDEKPEE 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.7%; Pred. No. 0..,
tive 32; Mismatches 108;
                                                              AYRYA-DLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                        PRT; 1849 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEGNIC PROJECT PA; 1.
PERMI, PF02225; PA; 1.
PERMI, PF00082; Peptidase_S8; 3.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00588; FLAGELLA_BB_ROD; UNKNOWN.
PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN.1
PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN.1
PROSITE; PS00138; SUBTILASE_RSP; 1.
SEQUENCE 1849 AA; 199014 WW; 219F0D44B
                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                        CELL ENVELOPE-ASSOCIATED PROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR003137; PA.
InterPro; IPR000209; Peptidase_S8.
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                                                                                                                                                        PRELIMINARY;
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Matches 76; Conserv
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01-DEC-2001
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Q9WZA6
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STRAIN=FCC1/HN;
Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M., Lu J.H., X J.;
"Molecular cloning and structure analysis of the Plasmodium falciparum
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STRAIN-MSBB / DSM 3109;
MEDLINE=99287316; PubMed=10360571;
MEDLINE=99287316; PubMed=10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
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Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
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Nature 399:323-329(1999).

EMBL: AE001738; AAD35722.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----EPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYAD 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 VVTRDGSVITLS-----PNNLDFSVKPGDVVNVKEFVPKKA---YVLGYVRN---PGLY 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FKGTFEKATS 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 EEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 -EKTEVYVSGYVSRPGVYEISPKENVTLEKLLSMAGG-----IKGTLEEVD-----SI
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ERYTHROCYTE MEMBRANE-ASSOCIATED GIANT PROTEIN ANTIGEN 332.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       992 AA; 109623 MW; 19291DDF29721BF3 CRC64;
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  Created)
Last sequence update)
Last annotation update)
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                                                                                     POLYSACCHARIDE EXPORT PROTEIN, PUTATIVE
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01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAX-2000 (TrEMBLrel. 13,
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 22.3
Matches 77; Conservative
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DNGEYTVDVADK - - - GYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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432 ALRSDLGAVQNRFNSAITNLGNTVN 456
                                                                                                                                                                                                                                                                                                                                                                                                          LLAKENG----KYTADLEDGGYTIN 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00223; Kunitz_BPTI.
InterPro; IPR000884; TSPI.
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Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS, PRO0759; BASICPTASE. SMART; SMO0408; IGC2; 2. SMART; SMO0131; KU; 10. SMART; SMO0209; TSP1; 7. SMART; SMO0217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 2.
Pfam; PF00014; Kunitz_BPTI;
Pfam; PF00095; wap; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 13, (TrEMBLrel. 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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LACUNIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000
01-MAY-2000
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                                                                                                                                                                12;
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STRAIN-SEROTYPE CHOLERAESUIS, ATCC 7001;
MEDLINE-9532531; Pubmed-7541401;
Vanegas R.A., Joys T.M.;
"Molecular analyses of the phase-2 antigen complex 1,2. . of Salmonella
                                                                                                                                                                                                                             ---TCEKKSVTKEIVDEVSR-TEEIVEENGSVTEGVDETG-----SVTEEIIE 2074
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                                                                                                                                                                Gaps
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erythrocyte membrane-associated giant protein Ag332 (Pf332) gene."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF202180; ARF15293.3; -.
InterPro: IPR001313; PUM.
SEQUENCE 5458 AA; 615269 MW; 4F6A37D92BDB0172 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  103 GKTQTAEFKGTFEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2075 BATVTEEVVEDGSVTEEVVEDGSVIQEVVEDGSVTEEIVQENGSVTEEIVEEEGSSV---
                                                                                                                                                                                                      ENKEET --- PETPETDSEEEVTIKANLIFANGSTQTAEF ---- KGTFEKATSEAYAYADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                163 EVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 AGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAY-RYADLLAKENGKYTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella cholerae-suis (Salmonella enterica).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118;
                                                                                                                         Length 5458;
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                                                                                                                    8.8%; Score 137.5; DB 5; Length 320.5%; Pred. No. 37;
ive 55; Mismatches 138; Indels
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Last annotation update)
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24.4%; Pred. No. 2.9;
ive 44; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
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01-NOV-1996 (TrEMBLrel. 01, Last and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DL-EDGGYTIN-'IRFAGKKVDEKPEE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Last and PHASE-2 FLAGELLIN STRUCTURAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 177:3863-3864(1995).
EMBL; U17175; AAC43352.1; -.
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InterPro; IPR001492; Flagellin_N.
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                                                                                                                                                              67; Conservative
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Best Local Similarity
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Matches 9
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SEQUENCE FROM N.A.
MEDLINE=99457716; PubMed=10528409;
Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
Expression of lacunin, a large multidomain extracellular matrix
protein, accompanies morphogenesis of epithelial monolayers in Manduca
                                                                                                                        312 ANGAELVKMSYTDKNGKTIDGGYALKAGDKYYAADYDEATGAIKAKTTSYTAADGTTKTA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 EEPKEEVTIKANLIYADGKTQTA-----EFKG--TFAEATAE-------AYRYAD 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Sphingiodea; Sphingidae; Sphinginae; Manduca.
264 TLA-AGATKT----TMPAG---ATTKTEVQELKDTPAVVSADAKNALIAGGVDATD
                                                                                        -----GKTQTAEFKGTFEEATAEAYRY-----ADALKKDNGEYTVDVADKGYTL
                                                                                                                                                                                                                                                                                                                                          -----YRYADLLAKE-NGKYTVDVADKGYTLNIKFA-------GKEKTP
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                                                                                                                                                                                                                 147 NIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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SIGNAL 1 21 POTENTIAL.
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EMBL: AF078161; AAF04457.1; -.
HSSP: P12111; 2KNT.
InterPro; IPR004094; Antistasin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 3198 AA.
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Pred. No. 30;
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24.8%;
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12;
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Qy <' 11 TPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKAT-SEAYAYADTLKKDNGEYTVDVAD 69

1028 TEESSVAEEETTK-----TTITEEVSGTSESASINSDKTTWTTLSEDTGKTSV--- 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 KGYTLNIKFAGKEKTPE-EPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADAL 128
Matches 70; Conservative 39; Mismatches 126; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 YADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLED 285
1234 ----TEEPTDVGS-SEAITSDKTTVSTASEETGKYSVSEEE 1269
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GenCore version 5.1.3
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OM protein - protein search, using sw model

October 29, 2002, 09:25:26; Search time 7.42896 Seconds (without alignments) 1589.653 Million cell updates/sec Run on:

US-08-325-278B-1 1565 1 AVENKEETPETPETDSEEEV......GGYTINIRFAGKKVDEKPEE 305 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	sta			salmone	P02565 gallus gall	rattus	P46821 homo sapien	_	. P37575 bacillus su	P19909 streptococc				P80544 staphylococ		_		P12839 rattus norv	_	pseudor		Q90339 cyprinus ca		_		٠,		_	P08799 dictyosteli		33	P43153 clostridium	P97794 mus musculu
SUMMARIES	a ID	L CNA_STAAU	1 EDC8_DAUCA	I DEXT_STRDO	FLJB	_			L MAPB_MOUSE	1 SP2B_BACSU	1 SPG2_STRSP	1 ICEV_PSESX	1 ICEN_PSESY	1 SSP5_STRGN	1 MRSP_STAAU	! ABPX_YEAST	1 NFM_MOUSE	1 NUCL_XENLA		1 SUBF_BACSU	1 ICEK_PSESX	1 NUCL_CHICK	1 MYSS_CYPCA	1 NFM_HUMAN	1 YF06_MYCPN	1 OSA7_BORBU	1 FLJB_SALAE	1 HAP_HAEIN	1 HAP1_HAEIN	1 MYS2_DICDI	1 SIAL_PIG	1 SLPO_BACBR	1 COLA_CLOPE	1 IRK8_MOUSE
	Length DB	1183 1	555 1				2459 1		2464]	332	593	1196	1200	1500	1637	627	848	650	845	1433	1148	694	1935	915	793	272	200	1394	1409	2116	300	1004	1104	424
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	Score		141	130.5	129	127.5	127	125	123.5	122	122	122	122	121.5	121.5	121	119.5		117.5	117.5	117	116.5	116.5	116	115.5	. 115	114.5	114.5	114.5	114	112.5	112.5	112.5	111.5
	Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25		. 27	28	29	30	31	32	33

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88888888

P43597 saccharomyc Q54114 streptococc	P48467 neurospora O53957 streptococc	Q62234 mus musculu	P05423 homo sapien	P16620 drosophila	P06176 salmonella	P13466 dictyostel1	Q28641 oryctolagus	
YFI6_YEAST TACY_STREQ	KINH_NEUCR TACY STRCB	MYM1_MOUSE	BN51_HUMAN	PTP6_DROME	FLIC_SALCH	GELA_DICDI	MYH4_RABIT	ABP2_HUMAN
	7	٦.		Н	Н	-1	Н	Н
1233 574	928	1666	395	1462	488	857	1938	2647
7.1	7.1	7.0	7.0	7.0	6.9	6.9	6.9	6.9
111.5	110.5	109.5	109.3	109	108.5	108.5	108.5	108.5
34	36	38	40	41	42	43	44	45

ALIGNMENTS

CINCINOTION	LLT 1 STAAU		(Rel.	(Rel. 37, Last	Ib-OCT-2001 (Ref. 40, Last annotation update) Collagen adhesin precursor	CNA.		Bacteria; Firmicutes; Bacillus/Clostridium group;	Bacillus/Staphylococcus group; Staphylococcus.		UENCE FI	STRAIN=FDA 574;	1=1311320;	Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,	4	expression of a gene encouring		[2]	ERRATUM.			J. Biol. Chem. 269:116/2-116/2(1994).			JINDIN-ED 01.	MEDILINE-9403.CACI; FUDMEDI-0120.09; Datti I M ROLOS I O HOPOPK M .	"Identification and biochemical characterization of the ligand		Biochemistry 32:11428-11435(1993).	[4]		MEDLINE=97475225; PubMed=9334749;	Symersky J., Patti J.M., Carson M., House-Pompeo K.,	Moore D., Jin L., Schneider A., Debucas L.J.,	•	aureus adhesin.";			COLLAGEN-CONTAINING SUBSTRATA.	-!- SUBCELLULAR LOCATION:	<u>.</u>	IN THE REGION OF THE MEMBRANE ANCHOR.
	RESU	01	D AC	IO	J C	G C	08	8	SSS	S Z	R.P.	2	Z	R.	X 5	7 6	R.	RN	RP	RA	RA	RL S	2 4	7 U	2 2	7 A	E	RT	RL	RN	RP	Z.	RA	KA G	5 5	RT	R	႘	ပ္ပ	ပ္ပင္ပ	၁ ဗ	ָ ט נ

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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGTTITNKY----TPGETSATVTKNWDDNNNQDGKRPTEIKVEL-YQDGKATGKTAILN 1039
                                                                                                     CYTOPLASMIC (POTENTIAL).
COLLAGEN-BINDING.
X 187 AA APPROXIMATE TANDEM REPEATS.
LYS/PRO-RICH (CELL WALL-SPANNING).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                     -----VTS 762
                                                                                                                                                                                                                                                                                                                                                                   124 Y-ADALKKDNGEYT-VDVADKG-----YT----LNIKFAGKEKTPEEPKEEVTIKAN 169
                                                                                                                                                                                                                                                                                                                                                                                       934
                                                                                                                                                                                                                                                                                                                                                                                                          ----YTVDVAD 213
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                   47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Spermatophyta; Spermatophyta; Core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus. NCBL_TaxID-4039;
                                                                                                                                                                                                                                                                                                     2 VENKEETPETPETDSE------EEVTIKANLIFANGSIQTAEFKGTFEKATS
                                                                                                                                                                                                                                                                                         -----EYTVDVADKGYTLNIKFAGKEKTPEEPKEE
                                                                                                                                                                                                                                                                                                                              ----IKANLIYADGKTQ------TAEFKGTFEEATAEAYR
                                                                                                                                                                                                                                                                                                                                                816 VTKNWDDNNNQDGKRPTEIKVEL-YQDGKATGKTAILNESNNWTHTWTGLDEKAKGQQVK
                                                                                                                                                                                                                                                                                                                                                                               ----TAEFKGTFAEATAEAYRY-ADLLAKENGKYTADLED---GGYTINIRFAGKKVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                               214 KGYTLNIKFAGKEKTPEEPKEEVT------IKANLIYADGKTQ----
                                                                                                                                                                                                               Length 1183;
                                                                                     EXTRACELLULAR (POTENTIAL). MEMBRANE ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                     713 VTNK-YTPETTSISGEKVWDDKDNQDGKRPEKVSV--NLLADGEKVKTLD-
                                                                                                                                                                                            B6A1CC072E575D76 CRC64;
                EMBL; M81736; AAA20874.1; -.
PDB; 1AMX; 24-JUN-98.
InterPro: IPR00118799; Gram_pos_anchor.
PROSITE; PS00343; GRAM, POS_ANCHORING; FALSE_NEG.
Signal; Repeat; Transmembrane; Cell wall; 3D-structure.
                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                123;
                                                                                                                                                                                                                                                                                                                                                                                                        170 LIYADGKTQTAEFKGTFEEATAEA---YRYADLLAKENGK--
                                                                            COLLAGEN ADHESIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Embryonic protein DC-8 (Clone 8/10).
                                                                                                                                                                                                              Score 151.5; DB Pred. No. 0.064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           555 AA
                                                                                                                                                                                                                                Mismatches
 send an email to license@isb-sib.ch)
                                                                                                                                                       PROTEINS
                                                                                                                                                                                            AA; 133066 MW;
                                                                                                                                                                                                                                                                                         EA---YAYADTLKKDNG-----
                                                                                                                                                                                                              9.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Daucus carota (Carrot).
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1177
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Matches 102;
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TRANSMEM
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SEQUENCE
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                                                                  SIGNAL
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                                                                                                                                                                                  PROTEIN BODIES, AND CELL WALLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 TLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKEN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 OKAAEAKDTTAOKA-----AEAKEKTGEYKDYAAOKAAEAKVLAAOKAAEAKDTTG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Gaps
                                                                                                                           MOI. Gen. Genet. 218:143-151(1989).
-!- FUNCTION: MAY PLAY A ROLE IN LATE EMBRYOGENY.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC, PROTEIN BODIES, AND CELL WAI
-!- SUGCTIC EMBRYO AND ENDOSPERM TISSUE.
-!- SIMILARITY: SOME, TO COTTON LEA D7, TO RAPE LEA 76, AND CARROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTTV---GKMTELKDSAADAARKAMDMFLGKKEEVKGKAGETAEAAKEKYEDTEFAARKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 KAKEYKEYAAQKAAEAKDATMQKTGEY-----KDYSAQKAAETKDATMEKTKE-----
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                                                       Franz G., Hatzopoulos P., Jones T.J., Krauss M., Sung Z.R.; "Molecular and genetic analysis of an embryonic gene, DC 8, from Daucus carota L.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X APPROXIMATE TANDEM REPEATS.
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STRAIN=CV. QUEEN ANNE'S LACE;
MEDLINE=89384429; PubMed=2571069;
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60260 MW;
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InterPro; IPR004238; LEA.
Pfam; PF02987; LEA; 6.
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Matches 78; Conser
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TFEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPE---EPKEEVTIKAN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mingorance J., Tanaka S., Tominaga A., Enomoto M.
                                                                                                                                                                                                                                                                                                                                                                    P52616; P97159;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 177:3863-3864(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95325331; PubMed=7541401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-37 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phase-2 flagellin.
FLJB OR H2 OR STM2771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=602;
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                                                                                                                                                                                                                                                                                                                                                         FLJB_SALTY
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                                                                                                                                                                                                                                                                                                                    RESULT 4
FLJB_SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
IN THE REGION OF THE MEMBRANE ANCHOR.
SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 DNGEYTVDV-ADK-----GYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EETPETPET-DSEEEVTIKANLI--FANGSTQ----TAEFKGTFEKATSEAYAYADTLKK 58
                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                STRAIN=6715 / UMB66;
MEDLINE-94292401; PubMed=8021165;
Wanda S.-Y., Curtiss R. III;
J. Bacteriol 176:3839-3850(1994)

J. Bacteriol 176:3839-3850(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Glycosidase; Signal; Transmembrane; Repeat; Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 130.5; DB 1; Length 1337; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (BY SIMILARITY).
MEMBRANE ANCHOR (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.3%; Score 1.v....
22.9%; Pred. No. 1.2;
+ive 51; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW; B494275A77A2E3D0 CRC64;
                                                                                                                                           01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-
                                                                                                                                                                                                                                           Streptococcus downei (Streptococcus sobrinus).
                                                                                          1337 AA.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 31-36.
STRAIN=6715 / UAB66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M96978; AAA21772.1; -.
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEXTRANASE.
                                                                                        PRT;
                                                                                                                          01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1337 AA; 143298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linkages in dextran. SUBUNIT: HOMODIMER.
                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1337
439 MEELKLQEEG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                       glucanohydrolase).
                                                                                                                                                                                                                                                                                               Streptococcus.
NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1333
                                                                                                                                                                                                                                                           Plasmid pYA902
                                                                                        DEXT_STRDO P39653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                        DEXT_STRDO
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                                                     RESULT 3
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-!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO FORM THE FILAMENTS OF BACTERIAL FLAGELLA.

-!- MISCELLANEOUS: INDIVIDUAL SALMONELLA SEROTYPES USUALLY ALTERNATE BETWEEN THE PRODUCTION OF 2 ANTIGENIC FORMS OF FLAGELA, TERMED PHASE-1 AND PHASE-2, EACH SPECIFIED BY SEPARATE STRUCTURAL GENES.
-!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY. "Complete genome sequence of Salmonella enterica serovar Typhimurium 170 LIYADGKTQTAEFKGTFEEATAEAY-RYA------DLLAKENGKYTVDVAD-KGYT 249 VRDADNNTLSEVNKAIAVESDWTKFPRYGIVGGSQDTNNSLLSKDADRYRAEIEKMKNMN LNIKF---AGKEKTPEEPKEEVTIKANLIYADGK---TQTA-EFKGTFAEATAEAYRYAD Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; MEDIINE-82049491; PubMed-6271461; Silverman M., Zieg J., Mandel G., Simon M.; "Analysis of the functional components of the phase variation ō Vanegas R.A., Joys T.M.; Mulecular analyses of the phase-2 antigen complex 1,2,. . . Salmonella spp." 271 LLAKENG------KYTADLEDGG-----YTINIRFAGKKVD 300 :||: | | |:: | | 369 ILAENTNTGEAPVLPETEYAYNSDDRGYGAQGQPMSYTVKIPKDGQEED 417 Cold Spring Harb. Symp. Quant. Biol. 45:17-26(1981).

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J. Biol. Chem. 262:6478-6488(1987).
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                                                                                                                                                                                                                                          light meromyosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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NP_BIND
DOMAIN
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MOD_RES
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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   NAMES OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
   and for commercial
                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 AVQSANSTNSQSDLDSIQAEITQRLNEIDRVSGQTQ---FNGV--KVLAQDNTLTIQVGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 DNGEYTVDVADK---GYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD------- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 NDGE-TIDIDLKQINSQTLGLDSLNVQKAYDVKDTAVTTKA---YANNGTTLDVSGLDDA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 ANGAELVKMSYTD----KNGKTIEGGYALKAGDKYYAADYDEATGAIKAKTTSYTAADGT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 TKTAANQLGGVDGKTEVVTIDGKTYNASKAAGHDFKAQPELAEAAAKTTENPLQKIDAAL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDIATE STATE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AVENKEETPETPETDS-EEEVTIKANLI-FANGSTQTAEFKGTFEKATSEAYAYADTLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 -----GKTQTAEFKGTFEEATAEAYRY-----ADALKKDNGEYTVDVADKGYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 AIKAATGGTNGTASVTGGAVKFDADNNKYFVTIGGFTGADAAK--NGDYEVNVATDG-TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : || || : | : | || 263 TLA-AGATKT-----TMPAG---ATTKTEVQELKDTPAVVSADAKNALIAGGVDATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 -----YRYADLLAKENGK-----YTVDVADKGYTLNIKFA------GK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 EKTPEEPKEEVTIKANLIYADGKTQTA-----EFKG--TFAEATAE-----AY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.2%; Score 129; DB 1; Length 505;
24.2%; Pred. No. 0.51;
ive 43; Mismatches 126; Indels 126;
   Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 NIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I -> S (IN REF. 3).
3A5CC404AF7AF88B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
1-FBE-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic.
   modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1940 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                         or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 RYADLLAKENG----KYTADLEDGGYTIN 291
                                  entities requires a license agreement
                                                                                                                                           EMBL, AE008826; AAL21657.1; EMBL, V01370; CAA24655.1; EMBL, 1026168; BAA05156.1; EMSL, 1026168; BAA05156.1; EMSL, 1026168; EMSC, 1198. InterPro; IPR001029; Flagellin_C. InterPro; IPR001029; Flagellin_N. Pfan; PF00060; Flagellin_N. Pfan; PF00669; Flagellin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00207; FLAGELLIN.
ProDom; PD000316; Flagellin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 37 I
505 AA; 52404 MW;
                                                                                                                        EMBL; U17177; AAC43354.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flagella; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
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P02565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INIT_MET
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus
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   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                HEAVY CHAIN SUBDUTING (MIG), 2 ALKALI LIGHT CHAIN SUBDUTING (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBDUTING (MLC-2).

-1 SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

-1 DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

-1 PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-1 MASCELLANGOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT EVERHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND 1 ROD-SHAPED
SEQUENCE OF 1502-1940 FROM N.A.
MEDLINE=83161144; PubMed=6833296;
Kavinsky C.J., Umeda P.K., Sinha A.M., Elzinga M., Tong S.W., Zak R.,
Jakovcic S., Rabinowitz M.; Wo types of embryonic myosin heavy chains
"Cloned mRNA sequences for two types of embryonic myosin heavy chains
from chick skeletal muscle. I. DNA and derived amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                        J. Biol. Chem. 258:5196-5205(1983).
-!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 123;
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ACTIN-BINDING.
ACTIN-BINDING.
MEHYLATION (FR.-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.1%; Score 127.5; DB 1; Length 1940;
21.6%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFRACMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G -> D.
T -> A (IN REF. 2).
ERA -> GRT (IN REF. 2).
MW; C34833D75B04DFF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQ.
COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, PO8799, IMMN.
InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222816 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00612; 10; 2.
Pfam; PF0063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01776; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYOSINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; V00430; CAA23712.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, J02714, AAA48972.1; -. PIR, A02990, A02990.
PIR, A29320, A29320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.6%;
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Best Local Similarity 21.0.
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ProDom; PD000355;
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us-08-325-278b-1.rsp

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1120 IEELEEEIEAERTSRAKAEKHRADLSRELEEISERLEEAGGATAAQIDMNKKREAEFQKM 1179
                                                                                                  1416 CASLEKTKORLONEVEDLMIDVERSNAACAALDKKOKNFDKILSEWKOKYEETQAELEAS 1475
                                                                                                                                                                                             1240 MESVSKAKANLEKMCRSLEDQLSEIKTKEEEQQRTINDISAQKAR----LQTESGEYSRQ 1295
                                                                                                                                                                                                                                                                         1296 VEEKDALISQLSRGKQAFTQQIEELKRHLEEEIKAKKCPAHALQSARHDCDLLREQYEEE 1355
                                                                                                                                                                                                                                                                                                                                                     1356 QEAKGELQRALSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAEEHVEAVNSK 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAPB_RAT STANDARD; PRT; 2459 AA.
P15205; 062058; 09ER21; 090M92;
01-APP-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (Neuraxin) (Contains: MAP1
                                                                                                                                                       ----TIKANL-----IYADGKTQTAEFKGTFEEATAEAYRYADALKKDNGEYTVD 138
                                                                                                                                                                                                                                                                                                                                                                                         222 FAGKEKTPEEPKEEV-----TIKANLIYA--DGKTQT-----AEFKGTFAEATAE---- 264
                                                                                                                                                                                                                                      ----- EEPKEE 163
                                                                                                                                                                                                                                                                                                              164 VTIKANLIYADGK--TQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIK 221
                                                                             92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AYR----YADLLAKENGKYTADLEDGGYTINIRFAGKKVDE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Spinal cord;
MEDLINE-90059871; PubMed-2555150;
Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;
"Neuraxin, a novel putative structural protein of the rat central nervous system that is immunologically related to microtubule-
    -OTAEF---
                                                                         39 KGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end of the rat microtubule-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
domains on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain, and Glial tumor; MEDLINE-22347374; PubMed-1639092; Zaunner W., Kratz J., Staunton J., Feick P., Wiche G.; "Identification of two distinct microtubule binding dc recombinant rat MAP 1B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION
  ------SEEEVTIKANLIFANGST-
                                                                                                                                                                                                                                  139 VADKGYTLNIKFAGKE------KTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-142 FROM N.A.
TRAIN-SPREAUE-DAWLEY, TISSUE-TESTIS;
MEDLINE-96257242; PubMed-8666295;
Liu D., Fischer I.;
alsolation and sequencing of the 5' end of associated protein (MAPIB)-encoding CDNA.'
Gene 172:307-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [4]
DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.
MEDLINE-97405699; Pubmed=9260743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Cell Biol. 57:66-74(1992).
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2 VENKEETPETPETD-
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                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropan Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in o wa modified and this statement is not removed. Usage by and for commercia
can associate
                                                                                                                                cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                    DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
                                                                                                                                                                                                                                                                     -:- PTM: Phosphorylated.
-:- SIMILARITY: TO MAPIA.
-:- CAUTION: A C-terminal fragment of this protein (residues 1597 2459) was originally described as neuraxin in ref.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASIC, CONTAINS MANY
                                                                                       stabilizing microtubules.
--- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can ass with MAPIA and MAPIB proteins.
--- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.1%; Score 127; DB 1; Length 2459; 4.1%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M -> V (IN REF. 1).
T -> S (IN REF. 1).
R -> K (IN REF. 3).
L -> I (IN REF. 3).
WW, ZE3F6872DEDB8BA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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MAP1 LIGHT CHAIN LC1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3.7;
47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAP1B 10.
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MAP1B 2.
MAP1B 4.
MAP1B 4.
MAP1B 5.
MAP1B 6.
MAP1B 7.
MAP1B 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000102; MAP1B_neuraxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00414; MAP1B_neuraxin; 10.
PROSITE; PS00230; MAP1B_NEURAXIN; 8.
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X60370; CAC16162.1; -. EMBL; X16623; CAA34620.1; ALT_SEQ.
                                                                                                                                                                                                                                                               of MAP1B (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U52950; AAB17068.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269497
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                                                                                                                                           heart or muscle.
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Matches 80; Conserv
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2169
2459
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CHAIN
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NCBI_TaxID=10090;
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589
MIM; 157129;
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P14873;
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MAPB_MOUSE
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                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain
                                              SLYASLASEKVQSLE----GEKLSPKSDISPLTPRESSPTYSPGFSDSTSGAKESTAAYQ 1806
                                                                                                                        EEPSYTQDNDLSELISV--SQVEASPSTSSAHTPSQIASPLQE----DTLSDVVPPRDM 1750
                                                                                         1807 TSSSPPIDAAAAEPYGFRSSMLFDTMQHHLALSRDLTTSSVEKDNGCKTPGDFNYAYQKP 1866
                                                                                                                                                                   -EKTTKTPEDGGYSCEI----TEKTTRTPEEGGYSYEISEKT-----TRTPEVSGYT 1964
                                                                        GT----FEEATAEAYRYAD-----ALKKDNGEYTVDVADKGYT---LNIKFAGK 153
                                   61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIK-ANLIYADG------KTQTAEFK 111
                                                                                                                                                NGKYTVDVADKGYTLNIKFAGKEKTPEEPKE-----EVTIKANLIYADGKTQTAEFKGTF 258
EETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK - - - - - KDN
                                                                                                             EKTPEEPKE-----EVTIKANLI--YADGKTQTAEFKGTFEEATAEAYRYADLLAKE
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                 1965 YEKTERSRRLLDDIS--NG--YDDTEDGGHTL 1992
                                                                                                                                                                                      259 AEATAEAYRYADLLAKENGKYTADLEDGGYTI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of MAP1B (By similarity). SIMILARITY: TO MAP1A.
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                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Fetal brain;
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01-NOV-1995 (
16-OCT-2001 (
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MAP1B.
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- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BINDS TO AT LEAST
TWO TUBULIN SUBDATTS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS
MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 TQ-TAEFKGTFEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      713 VK------KEEKKEVKKEEKEPKKEIKK----LPKDAKKSSTPLSEAKKPAALK-- 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 VTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA 223
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                                                                                                                                                                                                                                                                                                                                                                                 LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SWISS WEBSTER; TISSUE-Brain; Bright 199094539; PubMed-21480963; Noble M., Lewis S.A., Cowan N.J.; "The microtubule binding domain of microtubule-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-ARR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))
[Contains: MAP1 light chain LCl].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 2468;
8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 125; DB 1; Length 24; Pred. No. 4.8; 40; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540839CBDF09D461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 GKEKTPEEPKEEVTIKANLIYA...-DGKTQTAEFKGTFAEATAEA
                                                                                                          MAP1 LIGHT CHAIN LC1
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                                                                                                                            MAPIB 1.
MAPIB 2.
MAPIB 3.
MAPIB 4.
MAPIB 6.
MAPIB 6.
MAPIB 9.
MAPIB 9.
MAPIB 10.
                                                                              Phosphorylation
     IPR000102; MAP1B_neuraxin.
                                                      9
MAP1B contains a repeated sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                  270618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAPIB OR MTAPIB OR MTAP5.
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us-08-325-278b-1.rsp

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16-OCT-2001 (Rel. 40, Last anno
Stage II sporulation protein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus sp. (strain G148)
                                                                                                                                                                                                                                                                                                                                                         132 PC
122 G-
35923 MW;
                                                                                                                                                                                                                                                                                                EMBL; L04519; AAB59026.1; -.
                                                                                                                                                                                                                                                                                                            Z99118; CAB14766.1; -.
                                                                                                                                                                                                                                                                                                                                   spoliB.
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Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                     PIR; C40646; C40646.
SubtiList; BG10912;
                                                                                                                                                                                                                                                                                                                                                                                 332 AA;
                                   Bacillus subtilis.
                                                                      NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                          112
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P19909;
                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 ----
                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                              DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules. PTM: LC1 IS COEXPRESSED WITH MAPIB. IT IS A POLYPEPTIDE GENERATED FROW MAPIB BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIB AND MAPIB. IT INTERACTS WITH THE AMINO-TERMINAL REGION
        SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPIA AND MAPIB PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LNIKFAGKEKTPEEPKEEVTIKANLIY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ADGKTQTAEFKGTFEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 KEEVTIKANLIYADGKTQT-AEFKGTFEEATAEAYRYADLLAKENGKYTVDV-ADKGYTL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ENKEETPE-----TPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTAINS MANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            662 ------EDKT-----PLKKDEKPRKEEV-KKEIKKEIKKEEKKEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FBD3DD99CFDBDA87 CRC64;
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                                                                                                                                                                                                                                                                                                                      CHAIN LC1
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(Rel. 30, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.9%; Score 123.5;
24.7%; Pred. No. 5.9;
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MAPIB 4.
MAPIB 5.
MAPIB 6.
MAPIB 7.
MAPIB 8.
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InterPro; IPR000102; MAPIB_neuraxin.
Pfam; PF00414; MAPIB_neuraxin; 10.
PROSITE; PS00230; MAPIB_NEURAXIN; 7.
                                                                                                                                                                                                                                                                                                                                            MAP1B 2
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STABILIZING MICROTUBULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 DTLKKDNGEYTVDVADKGYT-
                                                                                                                                                                                                                                    EMBL; X51396; CAA35761.1;
                                                                                                                  SIMILARITY: TO MAPIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      2009
                                                                                                                                                                                                                                                                                                           Repeat;
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1925
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1959
1993
2010
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589
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CHAIN
                                                                                                        OF MAP1B
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P37575;
01-0CT-1994
01-0CT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 DNGEYTVD-VADKGYTLNIKFAGKEKTPEEPK--EEVTIKANLIYADGKTQTAEFKGTFE 115
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Immunoglobulin G binding protein G precursor (IGG binding protein G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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; FBE12F83C7569A68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Margolis P.S., Driks A., Losick R., "Sporulation gene spoIIB from Bacillus subtilis."; J. Bacteriol. 175:528-540(1993).
-i- FUNCTION: INVOLVED IN ENDOSPORE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%; Score 122; DB 1; Lr
23.7%; Pred. No. 0.82;
iive 41; Mismatches 125;
                                                                                                                                                Firmicutes; Bacillus/Clostridium group;
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Last annotation update)
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                                                                                                                                                                                    Bacillus/Staphylococcus group; Bacillus
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STRAIN-168 / PY79;
MEDLINE-93123172; Pubmed-8419299;
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SEQUENCE
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                                                                                                                                                                                                  MEDLINE-88015586; PubMed-3658689;
Filpula D., Alexander P., Fahnestock S.R.;
"Nucleoide sequence of the protein G gene from Streptococcus GX7805,
and comparison to previously reported sequences.";
Nucleic Acids Res. 15:7210-7210(1987).
                                                                                                                                                                                                                                                                                                          MEDILINE-86300657; PubMed-3017704;
Guss B., Eliasson M., Olsson A., Uhlen M., Frej A.-K., Joernvall H., Flock J.-I., Lindberg M.;
Flock J.-I., Lindberg M.;
"Structure of the IgG-binding regions of streptococcal protein G.";
EMBO J. 5:1567-1575(1986).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLUIAR LOCATION: Type I membrane protein. Cell wall.
-!- SIMILARITY: TO OFHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNOGLOBULIN G BINDING PROTEIN G. EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Malakauskas S.M., Mayo S.L.;
"Design, structure and stability of a hyperthermophilic protein
variant ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal; 3D-structure.
                                                                                                                      Structure and evolution of the repetitive gene encoding
                                                                                             Olsson A., Eliasson M., Guss B., Nilsson B., Hellman U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALA-RICH.
3 X 37 AA REPEATS.
1-1.
1-2.
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EMBL; Y00428; CAA68489.1; -
EMBL; X04015; CAA27638.1; -
PIR; S00128; S00128.
PIR; A26314; A26314.
PIR; A26314; A26314.
INTERPO; IPR0012988; GA.
INTERPO; IPR0012989; Gram_pos_anchor.
INTERPO; IPR001049; IGG_bind_B.
Pfam; PF001468; GA; 3.
Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF00746; Gram_pos_anchor; 1.
PFNNTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Struct. Biol. 5:470-475(1998).
                                                                                                                                                 Eur. J. Biochem. 168:319-324(1987)
                                                                  STRAIN=G148;
MEDLINE=88029445; PubMed=3665928;
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-G148;
MEDLINE-98290449; PubMed-9628485;
                                                                                                                                                                                                                                                                                      SEQUENCE OF 114-593 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 371-427.
                                                                                                                                      streptococcal protein G
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593
567
588
593
111
111
290
215
                                                                                                           Lindberg M., Uhlen M.;
                                                     SEQUENCE FROM N.A.
                                                                                                                                                                           SEQUENCE FROM N.A.
                          NCBI_TaxID=1306;
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34
568
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69
104
179
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                                                                                                                                                                                                                                                                                                     STRAIN-G148;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                  18;
1-3.
2 X 55 AA REPEATS.
2 -1.
2 -2-1.
5 X 5 AA REPEATS OF [DE]-D-A-K-K.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBUNIT: MEMBRANE ENVIRONMENT ON AGGREGATION SEEMS TO BE REQUIRED FOR ICE NUCLEATION ACTIVITY.
-:- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-:- DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
-:- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 WIYDDATKTFTVTEKPEVIDASELTPAVTTYKLVI-----NGKT----LKG---ETTT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 PKTDTYK-----LILNGKT----LKG---ETTTEAVDAATAEKVFKQYANDNGVDGE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 YTVDVADKGYTLNIK---FAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAYRYADALK-----KDN---GEYTVDVADKGYTLNIK---FAGKEKTPEEPKEEVTIK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 ANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKEN---GKYTVDVADKGYTLN---IK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKTL--KGETTT---KAVDAETAEKAFKQ---YANDNGVDGVWTYDDATKTFTVTEMVTE 501
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 PETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK-----KDN---GE 62
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Schmid D., Pridmore D., Capitani G., Battistutta R., Neeser J.-R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas syringae,";
FEBS Lett. 414:590-594(1997).
-!- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CRYSTALLIZATION IN SUPERCOOLED WATER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 EAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular organisation of the ice nucleation protein InaV from
                                                                                                                                                                                                                                                                                                                                                                                                                  68;
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                                                                                                                                                                                                                                                                                                                                         Score 122; DB 1; Length 593;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                              87; Indels
                                                                                                                                                                                                                                                               048BAA760D5B2920 CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                  31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                            PROTEINS
                                                                                                                                                                                                                                                               63291 MW;
                                                                                                                                                                                                                                                                                                                                         7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 VPGDAPTEPEKPEASIPL 519
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                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                               593 AA;
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es 72; Conserv
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254
303
303
373
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559
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AC 03847
AC 03847
AC 03847
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DT 16-DEC
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FAMILY
  proteins.
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Lindow S.E., Lahue E., Govindarajan A.G., Panopoulos N.J., Gies D.;
"Localization of ice nucleation activity and the iceC gene product in
Pseudomonas syringae and Escherichia coli.";
Mol. Plant Microbe Interact. 2:262-272(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166
                                                                                                                                                                                                                                                                                                                                                                                                     SSLIAGYGSTOTAGFKSIMTAGYGSTQTAQERSDLVAGYGSTSTA-GYSSSLIAGYG--S 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 VDVADKGYTLNIKFAGKEKTPEEPKEEVT-----IKANLIYADGKTQTAEFKGTFE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 KANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFAE---ATAEAYRYADLLAKENGKYTADL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          996
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                               ---TSEAYAYADTLKKDNGEYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               769 TQTAGYGSTLTTGY-GSTQTAQENSSLTTGYGSTSTAGYSSSLIAGYGSTQTAGYESTL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EATAEAYRYADALKKONGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVT-----I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 ASSLIAGYGSTQTAGY----ESTLTAGYGSTQTAQENSSLTTGY---GSTSTAGFASSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green R.L., Warren G.J.; "Physical and functional repetition in a bacterial ice nucleation
                                                                                                                                                                                                                                                                                                                   88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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"A model of the three-dimensional structure of ice nucleation
                                                                                                                                                                                                                                                                      Length 1196;
                                                                                                                                                                                                                                                                                             ; Pred. No. 3.3;
33; Mismatches 110; Indels
                                                                                                                                                                                                 47 OCTAPEPTIDE PERIODICITY.
117991 MW: C9E9974CB1731E68 CRC64;
                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1200 AA.
                                                                                                                                                                                                                                                                                                                                                             24 ANLIFANGSTQTAEFK-----GTFEKA-----
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                        Score 122;
                                                                                                                                                    PROSITE; PS00314; ICE NUCLEATION; 42. Ice nucleation; Repeat; Outer membrane. DOMAIN 172 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                          Pfam; PF00818; Ice_nucleation; 61.
PRINTS; PR00327; ICENUCLEATN.
                                   EMBL; AJ001086; CAA04521.1; -.
HSSP; P06620; 11NA.
InterPro; IPR000258; Ice_nucleatn.
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                                                                                                                                                                                                                                                                      7.8%;
                                                                                                                                                                                                                                            Query Match
Quest Local Similarity 25.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 317:645-648(1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ice nucleation protein.
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                                                                                                                                                                                                                         SEQUENCE 1196 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        831 TA-----GSTQTAQERSDLVTGYGSTSTAGYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 NLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         861 SLIAGYGSTOTAGY----ESTLTAGYGSTOTAQENSSLTTGY---GSTSTAGFASSLIS
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      MOI. BIOI. 232://9-/1/(1999).
FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
                                                  CRYSTALIZATION IN SUPERCOLED WATER.

-! SUBCELLIZATION IN SUPERCOLED WATER.

-! SUBCELLIZATION OUTER membrane.

-! SUBCELLIZATION OUTER membrane.

-! CONSENSUS

OCTAREPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

-! SUBCELLAROSUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE J NUCLEATION PROFIEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.

-! SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APEPTIDE PERIODICITY.
E3BEAD4BEA67ABB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00818; Ice_nucleation; 61.
PRINTS; PR00327; ICENUCLEATN.
PROSTITE; PS00314; ICE_NUCLEATION; 40.
Ice nucleation; Repeat; Outer membrane; 3D-structure.
DOMAIN 176 1151 OCTAPEPTIDE PERIODICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 3.3; 33; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSP5_STRGN STANDARD; PRT; 1500 AA. P16952; 054184; 15.00-1990 (Rel. 15, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 8494lutinin receptor precursor (SSP-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.8%; Score 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000258; Ice_nucleatn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1200 AA; 118587 MW;
Biol. 232:709-717(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X03035; CAA26837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 24.2
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus gordonii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 11NA; 31-OCT-93.
PDB; 11NB; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A24405; A24405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     973 FLTAGY
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35;

Conservative

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16;
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                           114
                                                                                                                                                                                                                                                                                                                                                     MRSP_STAAU
                                                                                                                                                                                                                                                                                              329
    Matches
                                3
                                                                                        63
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                                                                                                                                                                                                                                                                                                       -1- FUNCTION: MAY BIND SIALIC ACID RESIDUES OF SALIVARY AGGLUTININ (SAG) IN A CALCIUM-DEPENDENT REACTION. THE INTERACTION OF SAG WITH ITS RECEPTOR IN VARIOUS CALL STREPTOCCCCI MODULATE BACTERIAL COLONIZATION OF ORAL TISSUE AND IS ASSOCIATED WITH REDUCED LEVELS
                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
DOMAIN: THE PR2 REGION, BY SIMILARITY WITH THE PROLINE RICH
MAD THE S.PYOGENES M6 PROTEIN AND STAPHYLOCOCCAL PROTEIN A,
HAY TRAVERSE THE CELL WALL PEPTIDOGLYCAN AND IS FOLLOWED BY
HYDROPHOBIC AA WHICH MAY FUNCTION TO ANCHOR THE PROTEIN TO THE
MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO-RICH (PR2)
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                         Demuth D.R., Golub E.E., Malamud D.; "Streptococcal-host interactions. Structural and functional analysis of a Streptococcus sanguis receptor for a human salivary glycoprotein.";
                                                                                                                                                                                                                                              "Tandem genes encode cell-surface polypeptides SspA and SspB which mediate adhesion of the oral bacterium Streptococcus gordonii to human and bacterial receptors."; Mol. Microbiol. 20:403-413(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TTO M POTEIN OF S.PYOGENES.
4 X APPROXIMATE TANDEM REPEATS, HR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPROXIMATE TANDEM REPEATS, PR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
W: DCF190E7D44D889F CRC64;
                                                                                                                                                                                                                 Demuth D.R., Duan Y., Brooks W., Holmes A.R., McNab R., Jenkinson H.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN THE REGION OF THE MEMBRANE ANCHOR.
SIMILARITY: BELONGS TO THE SPAP/SSP5/SPAR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGLUTININ RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00746; Gram pos anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Signal; Repeat; Calcium-binding; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A35186; A35186.
InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEINS
                                                                                                                                           Biol. Chem. 265:7120-7126(1990)
                                                                                                                                                                                                    MEDLINE-96310377; PubMed-8733238;
                                                                    MEDLINE=90236997; PubMed=2185241;
                                                                                                                                                                       REVISIONS, SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U40026; AAC44100.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1474
1495
1500
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950
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                                                                                                                                                                                                                                                                                                                                                                 DENTAL CARIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
Y
                                        SEQUENCE FROM N.A.
Streptococcus.
NCBI_TaxID=1302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1467
                                                                                                                                                                                      STRAIN-M5
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CA_BIND
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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Length 1500;

DB 1;

Score 121.5; 1 Pred. No. 4.5;

7.8%;

Query Match Best Local Similarity

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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell wall; Transmembrane; Antibiotic resistance; Glycoprotein; Repeat;
                                                                                                                    YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                        271 EAIKORNETAKATY-EAAMKOYE-ADLAAIKKANEDNDADYQAKLAAYOTELARVOKANA 328
                                                                            ETKDKGTATTATDNAQ----KQDEIKSDYAKQAEEIKTTTEAYKKEVAAHQAETDKINAE 169
                                                                                                                                                                                                                                                                                                                                                                                              141 X 2 AA TANDEM REPEATS OF D-[SAG].
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
  Gaps
                                    ENKEETPETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ISOLATE 1061;
Savolainen K., Kuusela P., Paulin L., Korhonen T.K.;
"Pls, a large repeat-rich surface protein of methicillin resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHICILLIN-RESISTANT SURFACE PROTEIN.
                                                                                                                                                                                                                                                                                    ---KTQTAEFKGTFEEATAEAYRYADLLA--KENGKYTVDVADKGYTLNIKFAGKEKTPE
                                                                                                                                                           170 N--KAADDKYQKDL-----KSHQEEVEKI------NTANATAKAEYEAKLAQYQ
                                                                                                                                                                                                                                           211 KDLATVKKANEDSQQDYQNKLSAYQTELARVQKANAEAKEAYEKAVKENTAKNEALKVEN
                                                                                                                                                                                                     123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKE--EVTIKANLIYADG----
                                                                                                                                                                                                                                                                                                                                                                   231 EPKE--EVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKEN-----GKYTADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=96270743; PubMed-8665912;
Hilden P., Savolainen K., Tyynelae J., Vuento M., Kuusela P.;
"Purification and characterisation of a plasmin-sensitive surface
55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       676-682; 938-948; 1156-1168; 1176-1185;
Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75BE9ADB469BD309 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P80544; Q92F62;
01-FEB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MRZ-2002 (Rel. 41, Last annotation update)
Methicillin-resistant surface protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus/Staphylococcus group; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein of Staphylococcus aureus.";
Eur. J. Biochem. 236:904-910(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1637 AA; 174573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF115379; AAD09131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1199-1205 AND 1217-1224.
STRAIN-ISOLATE 1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
1637
1582
1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 624-628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1280;
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SGD; S0005765; ABP140.
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                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE FROM N.A., SEQUENCE OF 1-12; 38-72; 102-115; 244-286; 560-574 AND 598-608, FUNCTION, AND SUBCELLULAR LOCATION.
                                                                                                           63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                134 -----TEEAPKAEETDKATETAPKAEETDKAT-----TEEAPKAEETDKATEEAP 170
                                                                                                                                                                                                                                                           218 EKTATEEAPKTEETDKVETEEAPK----AEETSKAATEKAPKAEETN----KVETEEA 267
                                                                                                                                                                                                                                  123 RYADALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYA----D 174
                                                      Gaps
                                                                                        3 ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asakura T., Sasaki T., Nagano F., Satoh A., Obaishi H., Nishioka H., Imamura H., Hotta K., Tanaka K., Nakanishi H., Takai Y.; "Isolation and characterization of a novel actin filament-binding protein from Saccharomyces cerevisiae."; Oncogene 16:121-130(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLÜLAR LOCATION: Cytoplasm and cortical cytoskeleton. MISCELLANEOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
                                                                                                                                                                                                                                                                                                          175 GKTQTAEFKGTFEE---ATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            008641; 008644;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-MRR-2002 (Rel. 41, Last annotation update)
Actin-binding protein ABP140.
ABP140 OR YOR239W/YOR240W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SETARINE-S286C / FY1679;
STRAINE-S288C / FY1679;
MEDLINE-971279: Pubwed-8972580;
BOYEr J., Michaux G., Fairhead C., Gaillon L., Dujon B.;
Sequence and analysis of a 26.9 kb fragment from chromosome XV of the yeast Saccharomyces cerevisiae.";
Yeast 12:1575-1986(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Binds F-actin and shows weak F-actin crosslinking
                    Length 1637;
                                                                                                                                                                                                                                                                                                                                                                                  232 PKEEVTIKANLIYADGKTQTAEFKGTFAEATA----EAYRYADLLAKE 275
                                                                                                                                                                                                                                                                                                                                                                                                                    268 PAAEETNKA----ATEETPAVEDTNAKSNSNAOPSETERTOVVDTVAKD 312
         7.8%; Score _ 27.3%; Pred. No. 4.9; ...e. 20; Mismatches 111; ...e. 20; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 275147; CAA99460.1; ALT_SEO.
EMBL; 275147; CAA99461.1; ALT_SEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98127445; PubMed=9467951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOR LEU-276 AND GLY-277.
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
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12;
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                                                                                                                                                                                                                                                                                                                                                                          63 YTVD---VADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKT------QTAEF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 ESANNASEPAEEYSQSEEDADIE------QSNGKETENAENASQQANDGSTSTTTSK 214
                                                                                                                                                                                            4 NKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKK-DNGE 62
                                                                                                                                                                                                                171 IYADGKTQTA-EFKGTFEEATAEAYRYADLLAKENGKYTVDV-----ADKGYT-----L
                                                                                                              Length 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKKKKNKKKKKKKRNGNVNTNANV --- DDSTKTGENDDTTGDTTS 256
                                                                          627 AA; 71354 MW; D4E55F9485412F39 CRC64;
                52; Mismatches 103;
                                                                                                              Score 121; DB 1;
Pred. No. 1.9;
                                                                                                                7.7%; Score 121;
InterPro; IPR001601; Meth-transf.
InterPro; IPR000051; SAM_bind.
                                                                                                                                22.5%;
                                                                                                                                                      Conservative
                                                                                                                                Best_Local Similarity
Matches 64; Conserv
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                                                        INIT_MET
SEQUENCE
                                                                                                                Query Match
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Search completed: October 29, 2002, 09:29:54 Job time : 14.429 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 29, 2002, 09:27:36; Search time 12.7943 Seconds (without alignments) 2290.646 Million cell updates/sec Run on:

Title: Perfect score:

US-08-325-278B-1 1565 1 AVENKEETPETPETDSEEEV......GGYTINIRFAGKKVDEKPEE 305 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	.y ch Length DB ID Description	:	719 2 A42808	992 2 S54396	74 2 A34483 ig light c	664 2 S42574	479	A42404 colla	2 H84782	2 JC6171		2 S04909	2 E72350	2 н81070	7	2 T28680	~	2 E89824 hypothetical pro	1337 2 T30291 dextranase -	938 2	843 2 S72375	1940 2	863 2 S06017	913 2	2364 2 A56577	1035 2	955 2 A60990 .	673 2	
ď	Query Match	100.0	99.7	78.4	11.0	10.7	10.6	9.7	9.6	9.5	9.0	9.0	8.8	8.5	8.4	8.4	8.3	8.3	8.3	8.2	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.0	
	Score	1565	1561	1226.5	171.5	167	166	151.5	151	149	141.5	141	137.5	132.5	131.5	131.5	130.5	130.5	130.5	128.5	127.5	127.5	127	127	127	126.5	126	125.5	
	Result No.		7	9	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	• 23	24	25	26	72	

surface-located me	hypothetical prote	cyst germination s	ladder protein - C	microtubule-associ	hypothetical prote	EF protein - Strep	myosin heavy chain	surface exclusion	myosin heavy chain	probable peptidogl	endospore developm	hypothetical prote	protein G precurso	ice nucleation pro	probable cell surf
JC6009	D89808	T31108	T42223	QRMSP1	T39577	533441	S52696	S22452	S24348	AF1450	C40646	G86287	S00128	SNPSO	AD1525
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1302	495	1489	1198	2464	569	1822	698	890	955	1993	332	384	593	1200	657
8.0	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.8	7.8	7.8	7.8.	7.8	7.8	7.8	7.8
124.5	124	124	123.5	123.5	123	123	122.5	122.5	122.5	122.5	122	122	122	122	121.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 A4506 A4506 A4506 A4506 A4506 A4506 A4506 A4506 A5606 A5606 B5606 B5606

RESULT 2

142808
Ig light chain-binding protein precursor - Peptostreptococcus magnus
N.Alternate names: protein C.Species: Peptostreptococcus magnus
C.Species: Peptostreptococcus magnus
C.Species: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

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C;Accession: A34483
R;Akerstroem, B.; Bjoerck, L.
A;Tile: Protein L: an immunoglobulin light chain-binding bacterial protein. Characte A;Recession: A34483; MUID:90062074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Streptococcus dysgalactiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-May-2000
C;Accession: S42574
R;Jonsson, H.; Mueller, H.P.
Eur. J. Blochem. 220, 819-826, 1994
A;Title: The type-III Fo receptor from Streptococcus dysgalactiae is also an alpha(2)
A;Reference number: S42574; MUID:94192673
A;Accession: S42574
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig light chain-binding protein L - Peptostreptococcus magnus (fragments) C;Species: Peptostreptococcus magnus C;Species: 07-Sep_1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-1996
                                          EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                                                                                                                       180 AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT 237
                                                                                                                                                                                                                                                 238 IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --TFEEATAEAYRYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Moleoule type: DNA
A;Residues: 1-664 <20N>
A;Cross-references: EMBL:229666; NID:9470220; PIDN:CAA82764.1; PID:9470221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVD 66
                                                                                                                                                                                            YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE---KTPEEPKEEVTIKANLIYADGKTQT
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J.00038;
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Pred. No. 0.000
5; Mismatches
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Local Similarity 58.2%;
les 39; Conservative
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A;Residues: 1-74 <AKE>
C;Keywords: immunoglobulin
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Best Local Similarity
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EALKNDD 72
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                                                          repeated immu
                                                                                                                                                                                    R;Kastern, W.; Holst, E.; Nielsen, E.; Sjoebring, U.; Bjoerck, L.
Infect. Immun. 58, 1217-1222, 1990
A;Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence A;Reference number: A41493; MUID:90215984
A;Accession: A41493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S54396
R; Murphy, J.P.; Duggleby, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward, Mol. Microbiol. 12, 911-920, 1994
A; Title: The functional units of a peptostreptococcal protein L.
A; Reference number: S54396; MUID:95020613
A; Accession: S54396
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A;Variety: strain 3316
C;Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAE 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL:L04466; NID:q150673; PIDN:AAA67503.1; PID:q150674
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               R; Kastern, W.; Sjoebring, U.; Bjoerck, L.
J. Biol. Chem. 267, 12820-12855, 1992
A; Title: Structure of peptostreptococcal protein L and
A; Reference number: A42808; MUID:92316971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                           99.7%; Score 1561; DB 2;
100.0%; Pred. No. 5.8e-85;
iive 0; Mismatches 0;
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79.9%; Pred. No. 4.6e-65;
tive 22; Mismatches 31
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Best Local Similarity 79.99
Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 304; Conservative
                                                                                                            A;Status: preliminary
A;Molacule type: DNA
A;Residues: 1.719 <KAS.
A;Cross-references: GB:M86697
C; Accession: A42808; A41493
                                                                                                                                                                                                                                                                                A Status: preliminary
A:Molecule type: DNA
A:Residues: 202-275 <KA2>
C:Keywords: immunoglobulin
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C; Species: Staphylococcus aureus
C; Species: Staphylococcus aureus
C; Date: 04 Mar. 1993 Maguenoe_revision 18-Nov-1994 #text_change 10-Nov-1995
C; Accession: A44404; S27665
R; Patti, J.M.; Jonsson, H.; Guss, B.; Switalski, L.M.; Wiberg, K.; Lindberg, M.; Hook
B; Patti, J.M.; Jonsson, H.; Guss, B.; Switalski, L.M.; Wiberg, K.; Lindberg, M.; Hook
A; Title: Molecular characterization and expression of a gene encoding a Staphylococcu
A; Reference number: A42404; MUID:92165839
A; Contents: FDA 574
A; Accession: A42404
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             late embryogenesis abundant protein (AtECP63) [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Moleoule type: DNA
A;Residues: 1-448 <STO>
A;Cross-references: GB:AE002093; NID:g4415909; PIDN:AAD20140.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1042 ESNNWTHTWTGLDEKAKGQQVKYTVDELTKVNG-YTTHVDNNDMGNLIVTNKYTPKKPNK 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y-ADALKKDNGEYT-VDVADKG-----YT-----LNIKFAGKEKTPEEPKEEVTIKAN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         877 YTVEELTKVKGYTTHVDNNDMGNLIVTNKYTPETTSISGEKVWDDKDNQDGKRPEKVSVN 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLANGEKVKTL------DVTSETNWKYEFKDLPKYDEGKKIEYTVTEDHVKDYTTDI-- 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---EEVTIKANLIFANGSTQTAEFKGTFEKATS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETNWKYEFKDLPKYDEGKKIEYTVTEDHVKDYTTDI--NGTTITNKY-----TPGETSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TAEFKGTFEEATAEAYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EA---YAYADTLKKDNG------EYTVDVADKGYTLNIKFAGKEKTPEEPKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          818 VTKNWDDNNNQDGKRPTEIKVEL-YQDGKATGKTAILNESNNWTHTWTGLDEKAKGQQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIYADGKTQTAEFKGTFEEATAEA---YRYADLLAKENGK-----YTVDVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGYTLNIKFAGKEKTPEEPKEEVT-------IKANLIYADGKTQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TAEFKGTFAEATAEAYRY-ADLLAKENGKYTADLED---GGYTINIRFAGKKVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.7%; Score 151.5; DB 2;
23.8%; Pred. No. 0.15;
tive 45; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --IKANLIYADGKTQ------
                                                                                            Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-1185 <PAT>
A;Cross-references: EMBL:M81736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.7%
Best Local Similarity 23.8%
Matches 102; Conservative
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| PIYPEKPKD 1109
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R. Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, Mayer, K.F.X.
Bayer, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            late embryogenesis abundant protein-like - Arabidopsis thaliana
N;Alternate names: protein F8J2.210
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000
                                                                                                                                                                                179
                                                                                                                                                                                                                                       380
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                                                          VADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYR 123
                                                                                                                                                                                                                                                                                                                                                         437
                                                                                                                                                                                                                                                                                                                                                                                                                    296
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DAPELTPALTTYKLVVKGN-TFSGETTTKAIDTATAEKEFKQ-YATANNV---DGEWSYD
                                                                                                                                                                                                              269 DATKTFTVTEKPAVIDAPELTPALTTYKLIVKGNTF--SGETTT---KAVDAETAEKAFK
                                                                                                                                                                            -YADALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQT
                                                                                                                                                                                                                                                                                                  AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEV
                                                                                                                                                                                                                                                                                                                                                      381 KAIDAATAEKEFKQYATANGV---DGEWSYDDATKTFTVTEKPAVIDAPELTPALTTYKL
                                                                                                                                                                                                                                                                                                                                                                                                                    TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAG
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------MRLEGKKLDE 355
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A; Note: F8J2.210
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FTVTEKP 490
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Best Local S:
Matches 82,
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                                                          67
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C;Species: Petromyzon marinus (sea lamprey)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 151116
R;Jacobs, A.J.; Kamholz, J.; Selzer, M.E.
Brain Res. Mol. Brain Res. 29, 43-52, 1995
A;Title: The single lamprey neurofilament subunit (NF-180) lacks multiphosphorylation A;Reference number: 151116; MUID:95287814
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C;Species: Daucus carota (carrot)
C;Date: 28-Peb-1990 #sequence_revision 28-Peb-1990 #text_change 21-Jul-2000
C;Accession: S04909
R;Franz, G.; Hatzopoulos, P.; Jones, T.J.; Krauss, M.; Sung, Z.R.
Mol. Gen. Genet. 218, 143-151, 1989
A;Title: Molecular and genetic analysis of an embryonic gene, DC 8, from Daucus carot
A;Reference number: S04909; MUID:89384429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                              A;Residues: 1-1110 <JAC>
A;Cross-references: EMBL:U19361; NID:g632548; PIDN:AAA80106.1; PID:g632549
C;Superfamily: neurofilament triplet H protein
                               ---EPKEEV--TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLED 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGEYTVDVADKGYT------LNIKFAGKEKTPEEPKEEVTIKANLIYADGKT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTAEFKGTFEEATAEA-----YRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 PEE--PKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 GYTLNIKFAGKEKTPEEPK------EEVTIKANLIYADGKTQTAEFKGTFAEATAE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          685 ----VEAESKEEEEEDSKEADAEEDEAEEEEVKEEEVTKSDAEEAEAEAEEEAAKSEEE 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 SAEKDEEEEEEEEKEEEE -----AEAEEEEEDRGRKEGEAEAEEEEVEKEE 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  533 AEEAEVEEAEAEETEAEAAEEEEEAEGEEEAEAEGEEAEEAEEVEEEAIE------KA 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              639 EEEEABEBEEVISK-----KAKTQEAE----VEEBEAEA---AEAEAEEAEBAGEED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%; Score 141.5; DB 2;
25.4%; Pred. No. 0.54;
iive 38; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 AYRYA-DLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPEE
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 141;
                                                                                                                                     286 GGYTI-----NIRFAGKKVDEK 302
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Best Local Similarity 25.4.
Best Local Similarity 25.4.
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                                                                                                                                                                                                                                                                  RESULT 10
IS1116
NF-180 - sea lamprey
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C;Comment: This protein is a phosphotyrosine protein which belongs to late embryogenesis
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tate embryogenesis abundant protein - Arabidopsis thaliana
NyAlternate names: embryogenic cell protein 63; phosphotyrosine protein
C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 21-Jul-2000
C;Accession: JC6171 # F.; Komeda, Y.; Harada, H.; Kamada, H.
R;Yang, H.; Saltou, T.; Komeda, Y.; Harada, H.; Kamada, H.
A;Ritle: Arabidopsis thaliana ECP63 encoding a LEA protein is located in chromosome 4.
A;Reference number: JC6171; MUID:97169149
A;Accession: JC6171
A;Molecule type: mRNA
A;Residues: 1-448 cYAN>
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                                                                                                                                                                                                                                                                    79 EAAESTKEGAQIASEKAVGAK------DATVEKAKET----ADYTAEKVGE 119
                                                                                                                                                                                                                                                                                                                          63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                                                                          120 Y-----KDYTVDKAKEAKDTTAEKAKETANYTADKA-VEAKDKTAEKIGEYK----- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                   123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 ------DYAVDKA------VEAKDKTAEKAKETANYTADKA-KEAKDKTAEK 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 EAAESTKEGAQIASEKAVGAK-----DATVEKAKET----ADYTAEKVGE 119
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                                                                                                                                                              Gaps
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                                                                                                           Length 448;
                                                                                                      9.6%; Score 151; DB 2; Length 44 24.5%; Pred. No. 0.051; cive 38; Mismatches 107; Indels
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                                                                                                   Query Match
Best Local Similarity 24.5%
Matches 79; Conservative
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C; Keywords: seed
           A; Gene: At2g36640
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C; Genetics:
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Best Local Similarity 25.2%; Pred. No. 0.26; Matches 78; Conservative 30; Mismatches 130; Indels 72; Gaps 11; Qy 6 EPTPETDSEBEVIIKANLIFANGSTOTAEFKGTFEKATSEAYAYADTLK 57	QY 247 GKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLED 285
:: : :	RESULT 13 H81070
QY 58 KDNGETTVDVARKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQ-TAEFKGTFEE 116	lactoferrin-binding protein B NMB1541 [imported] - Neisseria meningitidis (strain MC5 C;Species: Neisseria meningitidis C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
Qy 117 ATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEBPKEEVTIKA 168 11	R. Tettellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. It, H.; Qin, H.; Vamathevan, J.; Glll, J.; Scarlato, V.; Masignani, V.; Pizza, M. ecione, 287, 1809-1815, 2000
Qy 169 NLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGY 216	A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Reference number: A81000; MUID:20175755
Qy 217 TLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKEN 276 1	A; Accession: mainly A; Status: preliminary A; Status: preliminary A; Molecule type: DNA A; Residues: 1-737 <tet></tet>
Qy 277 GKYTADLEDG 286 1 1 Db 439 MEELKLQEEG 448	A;Cross-reterences: GB:AEUU2504; GB:AEUU2098; NID:g/226/85; PIDN:AAF41896.1; PID:g/22 A;Experimental source: serogroup B, strain MC58 C;Genetics: A;Genetics: A;Gene: NMB1541
	Query Match 8.5%; Score 132.5; DB 2; Length 737; Best Local Similarity 22.8%; Pred. No. 1.1; Matches 85; Conservative 50; Mismatches 137; Indels 101; Gaps 17;
.nypothetical protein TM0638 - Thermotoga maritima (strain MSB8) C;Species: Thermotoga maritima C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: E72350	QY 5 KEETPETPET - DSEEEVTIK-ANLIFANGSTÇTAEFKGTFEKATSEAYAYADTLKKDN 60
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M. Nature 399, 323-329, 1999	7
A.Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A;Reference number: A72200; MUID:99287316 A;Accession: B72350 A;Status: preliminary	QY 108 AEFKGTFE
A; Molecule type: DNA A; Residues: 1-992 <arn> A; Cross-references: GB:AEO01738; GB:AEO00512; NID:g4981158; PIDN:AAD35722.1; PID:g498116 A; Experimental source: strain MSB8</arn>	Qy 139 VADKGYTLNIKFAGKEKTPEEPKEEVIIKANLIYADGKTQTAEFKGTFEEATAEA 193 1
A; Gene: TW0638 Query Match 8.8%; Score 137.5; DB 2; Length 992;	Qy 194YRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEV- 236 :: :: : : : : Db 316 DKEYLFFHTDADORLEGGFFGDNGEELAGRFISNDNSVFGVFAGKOKTFTENAADTK 372
Best Local Similarity 22.3%; Pred. No. 0.81; Matches 77; Conservative 40; Mismatches 112; Indels 117; Ga	
QY 2 VENKEETPETDSEEEVIKANLIFANGSTQTAEFKGTFEKATS 47 : : :: : :: 219 VLSKDETVEVSEKDIYQKNLLLKPGDTVHVQKIDERFAYVGAVARPGMYTFSRE 273	Db 373 PALSSGKHTKILDSLKISVDEASDKNPREFAISSMPDFGHPDKLLVEGREIPLVN 427 Qy 277 GKYTADLEDGGYT 289
QY 48 EAYAYADTLKKDNGEYTVDVADKGYTLNIKFAG 80	bb 428 KEQTIELADGRKT 440
Qy 81 KEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYAD 126	RESULT 14 441652 1341642 130K surface exclusion protein Sec10 precursor - Enterococcus faecalis plasmid pCF10 C; Species: Enterococcus faecalis
Qy 127 ALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTF 186 127 ALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTF 186 379 VVTRDGSVITLSPNNLDFSVKPGDVVNVKEFVPKRAYVLGYVRNPGLY 426	C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Oct-1999 C;Accession: 641662 R;Kao, S.M.; Olmsted, S.B.; Viksnins, A.S.; Gallo, J.C.; Dunny, G.M. J. Bacteriol. 173, 7650-7664, 1991
Qy 187 EEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKPAGKEKTPEEPKEEVTIKANLIYAD 246	A;Title: Molecular and genetic analysis of a region of plasmid pCF10 containing posit terococcus faecalis. A;Reference manner: A41662; MUID:92041679 A;Accession: G41662 A;Status: preliminary

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A; Mol A; Res	C; Gen A; Gen	Que	Mat	QY Dp	Qy	Q7 Dp	Qy Dp	Qy Dp	Qy Dp	RESULT 15 T28680 C; Date: 15 C; Date: 16 C; Accessing R; Joace 16 C; Accessing R; A	g .

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1 AVENKEETPETPETDSEEEV.......GGYTINIRFAGKKVDEKPEE
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/cgn2_6/prodata/1/iaa/6B_COMB.pep:*
/cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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ce 43, Applice 47, Applice 23, Applice 28, Applice 4, Applice 4, Applice 4, Applice 6, A		; Gaps	KKDN 60
ezunenbes ezunen	Z THEREOF.	Length 305; Indels 0;	ATSEAYAYADTLI
US-09-377-155-33 US-08-911-942-4 US-09-609-974-433 US-09-268-347-47 US-09-268-347-34 US-09-268-347-34 US-08-411-857-4 US-08-139-159-4 US-08-139-159-4 US-08-139-159-8 US-08-139-159-8 US-08-139-159-8 US-08-139-156-8 US-08-83-577A-155 US-08-83-577A-155 US-08-83-577A-155 US-08-83-577A-154 US-08-83-577A-154 US-08-83-577A-154 US-08-83-577A-154 US-08-83-577A-154	ALIGNMENTS 8795475 DNA Clouined SEC 2 EIN L AND HYBRID PROTEINS Tible Center, 701 Fifth Avenue Coster, 701 Fifth Avenue Coster, 701 Fifth Avenue (SAMS-DOS ease #1.0, Version #1.30 708/795,475 97 NS: 100084.402D1 1: 1: 1: 1:	Score 1565; DB 2; Pred. No. 1.6e-126; 0; Mismatches 0;	AVENKEETPETPETDSEEEVTIKANLIPANGSTQTAEFKGTFEKATSBAYADJLKKDN
2353 2353 2353 4 23553 4 1104 1104 272 337 272 337 337 337 404 404 411 411 411 411	ion US/0 i, Lars k, Lars N: PRO1F ES: 14 DORESS: 14 DORESS: 14 COMPA FORM: FO	100.0%; ty 100.0%; ervative	PETDSEEEVTIK
	75-1 1. Application 1. 5965390 INFORMATION: ANT: BJYTCK, L. OF INVENTION: OF INVENTION: OF SEQUENCES: ESSEE: SEED an ET: Gad Colum ET: Washigton TTY: USA 98104-7092 ER READABLE FOR UM TYPE: Flopp UM TYPE: Flopp UM TYPE: Flopp UM TYPE: READABLE FOR UM TYPE: READABLE FOR UM TYPE: READABLE SIFICATION UNABER: AMMONICATION NUMBER SIFICATION NUMBER: SIFICATION NUMBER: MARE: PATENTION NUMBER: SIFICATION NUMBER: SIFICATION NUMBER: COR CHARACTERIST TH: 305 amino acid NUMBENESS: UNKNOWN MUNDENNESS: UNKNOWN ILGOGY: UNKNOWN	n Similarity 05; Conserva	AVENKEETPET
116.5 116.5 116.5 116.5 116.5 116.1 115 115 115 115 115 115 115 115 115 1	GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: BJYTCK, Lar APPLICANT: SJYDFING; UTITE OF INVENTION: APPLICANT: SJYDFING; UTITE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: SEED and STREET: 6300 Columbi CITY: Seattle STREET: 6300 Columbi CITY: Seattle STREET: BARDABLE FORM: MEDIUM TYPE: FIOPPY COMPUTER: ASSIFICATION DAT ARELECTION NUMBER: FILING DATE: 11-FEB- CLASSIFICATION NUMBER: FILING DATE: 11-FEB- CLESTRATION NUMBER: TELEFONMUNICATION INFORMAT TELEFONMUNICAT	atc] 381	1 AVENE
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APPLICANT: Trowern, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Laurence, Oliver S.
APPLICANT: Duggleby, Clive J.
TITLE OF INVENTION: IMMUNGLOBULIN BINDING PROTEINS DERIVED
TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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6300 Columbia Center, 701 Fifth Avenue
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79.9%; Pred. No. 7.7e-97
Live 22; Mismatches 3
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APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
ATTORREY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGIETRATION UNMBER: 33,963
REFERENCE/DOCKET NUMBER: 1000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900 TELEFAX: (206) 682-6931 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 79.9%
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Washington
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ZIP: 98104
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                                1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN 60
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APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
APPLICANT: Sjvbring, Ulf
APPLICANT: Syvbring, Ulf
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
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APPLICATION NUMBER: US/08/795,475
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Pred. No. 2.7e-126;
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6300 Columbia Center, 701 Fifth Avenue
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Mismatches
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REFERENCE/DOCKET NUMBER: 100
TELECOMMUNICATION INFORMATION:
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TELEFAX: (206) 682-6031
INPERMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
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MEDIUM TYPE: Floppy disk
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Best Local Similarity
Matches 305; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98104-7092
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CITY: Seattle
STATE: Washingt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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| EKPEE 305
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                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-795-475-3
                                                                                                                                                                         181
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EATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYA 245
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                                                                                                         KDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Gaps
 2 ETPE--PEEEVTIKANLIFADGSTQNAEFKGTFAKAVSDAYAYADALKKDNGEYTVDVAD
                                                                                                                                                                                                                                                                 240 DGKTQTAEFKGTFEEATAEAYRYADLLAKVNGEYTADLEDGGYTINIKFAGK 291
                                                                                                                                                                                                                                               DGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK 297
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
ANDERGEBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
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Pred. No. 1.9e-45;
5; Mismatches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...nwg DATE: 26-MAR-1997
CLASSIFICATION: 435
TORNEY/AGENT ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08828741B Patent No. 6043069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Digiglio, Frank S. REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
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75.9%;
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Best Local Similarity 75.9
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garden City
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APPLICANT: Koentg
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STATE:
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                                                                                                       YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQT 179
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                                                                                                                                                                          AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT
                                                                                                                                                                                                                                           238 IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Atkinson, Anthory
APPLICANT: Murphy, Jonathan P.
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Duggleby, Clive J.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.7%; Score 1216; DB 4;
82.5%; Pred. No. 1.1e-96;
tive 20; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08446137B Patent No. 6162903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Trowern, Angus R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washington
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                ---EQPGE 578
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STREET: 63
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Best Local
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Sequence 13, Application US/08828741B
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US-09-160-567-13
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234 IKFAGKEATNRNTDGSTDYGILQINSRWGGLTSAEEVTIKANLIFANGSTQTAEFKGTFE 293
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Pred. No. 1.9e-45;
5; Mismatches 15; Indels
                                                                                                                                                                                                                                              APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CAPALYTIC ANTIBODIES AND A METHOD OF
                                       Qy - 116 EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPR 161

Db 294 KATSEXYAADTLKKDNGEYTVDVADKGYTLNIKFAGKESANRHPQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 KATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKESAWRHPQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPETWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: United States of America
ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELEPANTON: (516) 742-4346
TELEPANT: (516) 742-4346
TELEPANT: (516) 742-4346
TELEPANT: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                     Sequence 6, Application US/09160567
Patent No. 6326179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.5%;
75.9%;
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amino acid
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Best Local Similarity 75.9
Matches 126; Conservative
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                                                                                                                                                               US-09-160-567-6
                                                                                                                                              RESULT 6
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US-08-828-741B-13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAVADTLKKDNGEYTVDVADKGYTLNIK 77
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Pred. No. 1.4e-45;
5; Mismatches 14; Indels
                                              APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09160567
Patent No. 6326179
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlian, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              SEE: SCULLY, SCOTT, MURPHY & PRESSER: 400 Garden City Plaza Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1059
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEERAX: 23 091 SANS UR
INFORMATION FOR SEQ ID NO: 13:
                          Koentgen, Frank
Suess, Gabriele M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.3%;
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LENGTH: 178 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.3
Best Local Similarity 76.2
Matches 125; Conservative
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                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION:
APPLICANT: Koente
                                                                                                                                                                                                                                                                                     STATE: New York
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-----PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                 39.3%; Score 615; DB 3; Length 198; 76.2%; Pred. No. 1.6e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Koentgen, Frank
APPLICANT: Tariinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 TAEAYRYADALKKONGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: New Vor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
SOFTWARE: Patentin netters CURRENT APPLICATION DATE:
APPLICATION DATE: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELETS: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENDTH: 198 amino acids

LENDTH: 198 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: DiGigilo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09160567
Patent No. 6326179
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 76.2
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-828-7418-8
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US-09-160-567-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 615; DB 4; Length 178;
Pred. No. 1.4e-45;
5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinfon, David M.
APPLICANT: Tratlinfon, David M.
APPLICANT: Tratlinfon, David M.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                            ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                             United States of America
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08828741B Patent No. 6043069 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                          ATTONEX AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4346
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
  400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.3%;
76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 178 amino acids
amino acid
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Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-09-160-567-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                     Garden City
New York
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                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-828-741B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                             COUNTRY:
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                                        STATE:
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 IKFAGKEKTPEE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 125; Conser
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                  76 IKFAGKEKTPEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 11530
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                     Best Local Sin
Matches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
 Query Match
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                                                                                                                                                                                                                                                                 20; Gaps
                                                                                                                                                                                                                                                                                                                       32 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLIIK 91
                                                                                                                                                                                                                                                                                                      18 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
                                                                                                                                                                                                                            Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, David M.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            Score 615; DB 4;
Pred. No. 1.6e-45;
                                                                                                                                                                                                                                               Pred. No. 1.6e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08828741B Patent No. 6043069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 1059
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
           TELEPHONE: (516) 742-4343
- TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAN: (516) 742-4343
TELEFAX: (516) 742-4366
TELEEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            39.3%;
76.2%;
                                                                                                           LENGTH: 198 amino acids TYPE: amino acid
                                                                                                                                                                                                                        Query Match 39.3
Best Local Similarity 76.2
Matches 125; Conservative
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                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-160-567-8
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STATE: New York
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US-08-828-741B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PKEEVTIKANLIYADGKTQTAEFKGTFE 115
                                                                                                                        |||||||| |
234 IKFAGKEATNRNIDGSTDYGILQINSRWGGLTSAEEVTIKANLIFANGSTQTAEFKGTFE 293
                                                                                               16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                   20;
Score 614; DB 3; Length 495; Pred. No. 6.8e-45; i Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
                                                                                                                                                                                                                                                                                                                    294 KATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKE 332
                                                                                                                                                                                                                                                                                         116 EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 614; DB 4;
Pred. No. 6.8e-45;
4; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09160567 Patent No. 6326179 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Diciglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/POCKET NUMBER: 1059
TELECOMMUNICATION INFORMATION:
  39.2%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.2%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELER: 230 901 SAS UR
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 495 amino acids amino acids
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 182;
                                                                                                                                                                                                                          APPLICANT: Koencen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Tarlinton, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 613; DB 3; Length 182
Pred. No. 2.1e-45;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
                                                                     294 KATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKE 332
                                                     EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 EEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAG 152
                                                                                                                                                                                                                                                                                                                                                                                                                           New York : United States of America
                                                                                                                                                                         Sequence 2, Application US/08828741B Patent No. 6043069 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: DIGGGILO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
TELERA: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Séquence 2, Application US/09160567
Patent No. 6326179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.2%;
78.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                         Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                         RESULT 13
US-08-828-741B-2
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CITY: Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-160-567-2
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75 NIKFAGKEKTPEEP-------KEEVTIKANLIYADGKTQTAEFKGTF 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Trowern, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Duggleby, Clive S.
APPLICANT: INWINDING PROFEINS DERIVED
TITLE OF INVENTION: PROM L PROTEIN AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 182;
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYETEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.2%; Score 613; DB 4; 78.5%; Pred. No. 2.1e-45; Live 5; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 EEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-434
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-446-137B-8
; Sequence 8, Application US/08446137B
; Patent No. 6162903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 182 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 78.5
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                       STREET: 400 Garden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                COUNTRY: UN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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1;

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Length 75;
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIF: 98104
COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: LOWER: LOWERSE: BATENING SYSTEM:
COMPUTER: IBM PC Compatible
COMPUTER: LOWERS: LOWERS: 13.0
COMPUTER: LOWERS: 10.0
COMPUTER: LOWERS: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 334; DB 4;
Pred. No. 4.5e-22;
4; Mismatches 3.
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Best Local Similarity 90.1%;
Matches 64; Conservative
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287 GYTINIRFAGK 297 . **q**0 ò

Search completed: October 29, 2002, 09:31:54 Job time: 11.4926 secs

0;

0; Gaps

3; Indels

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model
                                              Run on:
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October 29, 2002, 09:25:06; Search time 23.9378 Seconds (without alignments) 1415.233 Million cell updates/sec

Title:

US-08-325-278B-1 1565 1 AVENKEETPETPETDSEEEV.......GGYTINIRFAGKKVDEKPEE 305 Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

747574 Total number of hits satisfying chosen parameters: 747574 seqs, 111073796 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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| SIDSI/gcgdata/geneseq/geneseqp-emb1/Aa1993.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-emb1/Aa1995.DAT:*
| SIDSI/gcgdata/geneseqfyeneseqp-emb1/Aa1995.DAT:* /SIDS1/gcgdata/geneseq/geneseqp.embl/AA1997.DAT:*/SIDS1/gcgdata/geneseq/geneseqp.embl/AA1999.DAT:*/SIDS1/gcgdata/geneseq/geneseqp.embl/AA1999.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* A_Geneseq_032802:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Immunoglobulin lig	Sequence encoding	Amino acid sequenc	Expression vector	Protein L. Peptoc	Protein L. Peptoc	Immunoglobulin bin	Growth factor TLHL	TLHL amino acid se	Growth factor LHL-	Amino acid sequenc
ES	<	ğ	7			9	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ğ							
SUMMARIES			<u>a</u>		AAR42993	AAR42994	AAB31372-	AAB10432	AAR42203	AAR43699	AAR42204	AAW32482	AAY06909	AAW32486	AAY06913
			DB	:	14	14	22	21	14	14	14	18	20	18	20
			Match Length DB		305	434	467	367	1027	1027	291	342	342	178	178
	æ	Query	Match	1 1 1 1 1 1 1	100.0	100.0	98.7	87.3	78.4	78.4	77.7	39.5	39.5	39.3	39.3
			Score		1565	1565	1544.5	1366	1226.5	1226.5	1216	618	618	615	615
		Result	No.		7	7	e	4		ø	7	80	6	10	11

Growth factor LHL.	1 fact	CATAB-TEV aminoaci	Growth factor LHL	LHL growth factor	Amino acid sequenc	Peptostreptococcus	Peptostreptococcus	Peptostreptococcus	Peptostreptococcus	Ig light chain bin	tostrept	PpL mutant protein	mutant	mutant	nutant	u	Peptostreptococcus	Peptostreptococcus	S. dysgalactiae MI	Collagen binding p	A. thaliana enviro	Enterococcus faeca	Enterococcus faeca	Enterococcus faeca	Amino acid sequenc	S. aureus SdrE pro	N-terminal truncat	Choline binding pr	N-terminal region	N-terminal choline	no acid	C3 binding protein
AAW32481 AAY06910	AAW32480	AAY06908	AAW32479	AAY06907	AAY06915	AAY82537	AAY82538	AAY82540	AAY82539	AAY82536	AAY82544	AAY82545	AAY82548	AAY82546	AAY82547	AAY82542	AAY82543	AAY82541	AAR71929	AAR22675	AAY77965	AAY00138	4	AAY00142	AAY49150	AAY08643	AAY49231	AAY32103	AAY49247	AAY32186	AAY49144	AAW62654
18	18	20	18	20	20	21	21	21	21	21	21	21	21	21	21	21	21	21	16	13	21	20	20	20	20	20	20	20	20	20	20	19
198	0	9	8	182	ω	9/	72	72	72	82	75	82	82	82	82	7.1	74	71	664	1185	448	1638	1638	1638	414	1166	376	376	413	413	414	564
	39.2									21.8	21.3	21.3	21.3	21.2	21.0	20.2	19.6		٠.		9.5		9.0	9.0	8.4			8.3				8.3
615	614	614	613	613	809	389	371	370	369	341	334	334	334	332	328	315.5	306	303	167	154.5	149		4		131.5						130.5	130.5
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAR42993 standard; Protein; 305 AA. (first entry) 16-MAY-199 10 PR4 2993 RESULT 1 AAR42993

Immunoglobulin light chain binding protein (Protein L).

Immunoglobulin; light chain; binding; identification; purification; separation.

E. coli LE392/PHDL, DSM 7054.

Location/Qualifiers 5..305 /label= Bl immunoglobulin light chain binding 81.305 /label- B2 immunoglobulin light chain binding domain. Domain Domain Key

/label= B3 immunoglobulin light chain binding /label= B4 immunoglobulin light chain binding domain. domain. domain. 225..305 153..305 Domain Domain

297...305 /label= B5 immunoglobulin light chain binding domain.

W09322342-A

Domain

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/label= B1 immunoglobulin light chain binding
                                                        /label= B2 immunoglobulin light chain binding
                                                                                     /label= B3 immunoglobulin light chain binding
       Location/Qualifiers
                                                                                                domain.
                                                                   domain.
                                     domain
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Best Local Similarity 100.
Matches 305; Conservative
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                                                                                                                                                                  309..434
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                                             81..305
                                                                                                                                                                                                                                                                                                                                                                     Sjoebring
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-368722/46.
P-PSDB; AAR42994.
                                                                                                                                     297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 AA;
                                                                                                                                                                                                                                                                                                            28-APR-1993;
                                                                                                                                                                                                                                                                                                                              28-APR-1992;
                                                                                                                                                                                                                                                                   W09322342-A
                                                                                                                                                                                                                                                                                                                                                                     Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
        Key
Domain
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                                                                                                                                                                                                                                                                                                                                                                                        61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120
                                                                                                                                                                                                                                                                                                                                                                                                                   AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300
                                                                                                                                                                                             light chains. It is useful for binding, separating (purifying) and identifying immunoglobulin and for removing immunoglobulin molecules from serum. Hybrid proteins of the L protein can bind all human immunoglobulin classes and many immunoglobulins from other species. They are highly soluble and retain their binding activity at high without loss of activity.
                                                                                                                                                                                                                                                                                                                                                 1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYADTLKKDN 60
                                                                                                                                                                                                                                                                                                                                        1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin; light chain; binding; identification; purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein (Protein L) is capable of binding to immunoglobulin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA
                                                                                                                           protein L binding light chains of all immunoglobulin classes
                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                DB 14; Length 305;

    for binding purifying and identifying immunoglobulin, also
related DNA, vectors and host cells

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoding immunoglobulin light chain binding protein.
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                100.0%; Score 1565; DB 14; 100.0%; Pred. No. 2.2e-110;
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR42994 standard; Protein; 434 AA.
                                                                                                                                                                  Claim 1; Page 36; 71pp; English.
                                                                                                                                                                                                                                                                                                                    ;
0
                                                       (HIGH-) HIGHTECH RECEPTOR AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli L392/PHDLG, DSM 7055
                                   92SE-0001331.
                 93WO-SE00375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 305; Conservative
                                                                         Sjoebring
                                                                                            WPI; 1993-368722/46.
N-PSDB; AAQ50452.
                                                                                                                                                                                                                                                                            305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIIII
EKPEE 305
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                28-APR-1993;
                                   28-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    separation;
                                                                          Bjoerck L,
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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AAR42994
                 δ
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61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120 121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180 Protein L (AAR42993) is capable of binding to immunoglobulin G light chains. It is useful for binding, separating (purifying) and identifying immunoglobulin and for removing immunoglobulin molecules from serum. This is the coding sequence of one hybrid protein of the L protein. The hybrid proteins can bind all human immunoglobulin classes and many immunoglobulins from other species. They are highly soluble and retain their binding activity at high without loss of activity. Gaps 9 1 AVENKEETPETDSEEEVTIKANLIFANGSTOTAEFKGFFEKATSEAYAVADTKKDN 1 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN New protein L binding light chains of all immunoglobulin classes - for binding purifying and identifying immunoglobulin, also related DNA, vectors and host cells ; Length 434; /label= C2 immunoglobulin heavy chain binding /label= B4 immunoglobulin light chain binding /label= B5 immunoglobulin light chain binding /label= C1 immunoglobulin heavy chain binding /label= D intermediate immunoglobulin heavy Indels 100.0%; Score 1565; DB 14; 100.0%; Pred. No. 3.4e-110; ive 0; Mismatches 0; chain binding domain Claim 6; Page 39-40; 71pp; English domain. domain domain domain

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Indels

Length 467;

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Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with antibody library -
                                                                                                                                                                                                                                                                                                     100 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 EFKGTFEEATAEAYRYADLL-AKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIK 239
                                                                                                                                                                                                     40 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYEXADTLKKDN
                                                                                                                                                                                                                                                                                                                                                                                                          160 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AVENKEETPETPETDSEEEVTIKANLIFANGSTOTAEFKGTFEKATSEAYAYADTLKKDN
                                                                                                                                                                                                                                                                           61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE
                                                                                                                                                                                                                                                                                                                                                                             121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKV
                                                                        Score 1544.5; DB 2.
Pred. No. 1.3e-108;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moldenhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression vector pSEX11L4 protein G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB10432 standard; Protein; 367 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Fig 1; 22pp; German.
                                                                        98.78;
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                                                                                                                            Conservative
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N-PSDB; AAA71428.
                                                                        Query Match
Best Local Similarity
Matches 303; Conserv
                         467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 DEKPE 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Breitling F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-1999;
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                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a method for expressing and isolating a recombinant protein in a plant. The method comprising expressing a recombinant protein and a callulose fusion protein including the recombinant protein and a callulose binding peptide fused to it, where the fusion protein is compartmentalised and sequestered within plant cells, plant derived tissue or cultured plant cells. The method is useful for obtaining large quantities of the recombinant proteins and protein products in a simple and cost-effective manner. Recombinant proteins may be used commercially, such as in the food processing industry, e.g. glucoamylases and glucose such as in the food processing industry, e.g. glucoamylases and jlucose isomerases are used for converting starch to high fructose corn syrup, proteinases for the hydrolysis of high molecular weight proteins and in manufacturing leather or alcoholic beverages, pectinesterases for pectin hydrolysis in food industry, lipases for cleaving expert linkage in triglycerides, and for effluent treatment. The recombinant proteins may further be used to produce protein antibiotics, which can be used in triglycerides, and for effluent treatment. The recombinant proteins may further be used to produce animal feed enzymes. The present sequence represents a fusion protein of the invention, and comprises a fusion of a cell signal peptide, protein L, CBD cex, and an endoplasmic reticulum retaining peptide.
240
                                                                                               241 NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein production; food processing; protein antibiotic; feed enzyme; protein L: CBD cex protein; cell signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of protein L/CBD cex/ER retaining peptide fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressing and isolating recombinant protein in a plant, useful for producing large quantities of recombinant proteins, by expressing a fusion protein including a cellulose binding peptide fused to a recombinant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (XISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB31372 standard; Protein; 467 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0329234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-112219/12.
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                                                                                                                                                                                                                                                                           301 EKPEE 305
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20-APR-2001

AAB31372;

301

RESULT 3

21-DEC-2000.

Synthetic.

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invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) class I k(k) molecule; an antibody-binding site of proteins A, G, L or LG, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select MAD with specificity for particular antigens. MAD can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in MAD selection. This sequence represents the protein G contained in the expression vector pSEXILL4 which contains the protein G, Neo-R and the bla protein described in the method of the invention.
                                                                                                                                                                                                                                                                                             81 VDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRY 140
                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                                                                                                                                                                                                                            TFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIY 244
                                                                                                                                                                                                                                                                                                                                                                                        65 VDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRY 124
                                                                                                                                                                                                                                                                                                                              125 ADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTOTAEFKG 184
                                                                                                                                                                                                                                                  25 KEKTPEEP----KEEVIIKANLIYADGKTQTAEFKGTFEEATAEAYRYADALKKDNGEYT 80
                                                                                                                                                                                                                                    5 KEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYT 64
                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide; immunoglobulin; binding; analysis; purification; ELISA; enzyme linked immunoabsorbant assay.
                                                                                                                                                                                         Length 367;
                                                                                                                                                                                      87.3%; Score 1366; DB 21;
88.6%; Pred. No. 2.8e-95;
                                                                                                                                                                                                             15; Mismatches
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/label- Mature protein L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36..59
/label= Signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR42203 standard; Protein; 1027 AA
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92GB-0026928
                                                                                                                                                                                                             Matches 264; Conservative
                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptococcus magnus
                                                                                                                                                                  367 AA;
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24-DEC-1992;
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                                                                                                                                                                  Seguence
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                                                                                                                                                                                      Query Match
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180 AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                 L correspond to the repeated sequences inprotein L which bind immunoglobulin kappa light chains. They can be used in protein analysis, purification procedures and other blochemical processes e. BLISA. The synthetic molecules are of particular advantage if they are free of regions in protein L which exhibit albumin and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VENKEETPETPETPESEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG 61
                                                                                                                                                                                                                                               The synthetic immunoglobulin binding proteins derived from protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE---KTPEEPKEEVTIKANLIYADGKTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1027;
                                                                                                          New immunoglobulin binding proteins derived from Protein L - which bind immunoglobulin kappa light chains but not albumin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin; binding; immobilisation; light chains;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.4%; Score 1226.5; DB 14; 79.9%; Pred. No. 3.2e-84; ive 22; Mismatches 31; II
Trowern AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibodies; diagnosis; pharmaceutical; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 36..59 (Jabel= Signal sequence. 60..968 /label= Mature protein L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein L.
Murphy JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR43699 standard; Protein; 1027 AA.
                                                                                                                                                                                                   Disclosure; Figure 1; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
Duggleby CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                       1993-368798/46.
                                                                                                                                                                                                                                                                                                                                                                                                                           1027 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 KVDEKPEE 305
                                                            N-PSDB; AAQ50946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---EQPGE
Atkinson A,
                                                                                                                                                                                                                                                                                                                                                                                 binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9322438-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sin
Matches 246;
                                                                                                                                                      cell walls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR43699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
AAR43699
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us-08-325-278b-1.rag

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70 KGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADALK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFE 187
                                                                                                                                                                                                                                                                                                                                           L comprise repeated sequences from protein L which bind immunoglobulin kappa light chains. They can be used in protein analysis, purification procedures and other blochemical processes e. g. ELISA. The synthetic molecules are of particular advantage if they are free of regions in protein L which exhibit albumin and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVAD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The synthetic immunoglobulin binding proteins derived from protein
                                                                                                                                                                                                                       New immunoglobulin binding proteins derived from Protein L - which bind immunoglobulin kappa light chains but not albumin oʻr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catalytic antibody; growth factor; B-cell mitogenesis; TLHL; L protein; hen egg lysozyme; kappa light chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth factor TLHL (catalytic antibody precursor).
                                                                                                                                       Murphy JP, Trowern AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.7%; Score 1216; DB 1482.5%; Pred. No. 4.2e-84.ive 20; Mismatches 29
                                                                                                     (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Peptostreptococcus magnus.
Chimeric - Gallus sp.
Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                             Claim 12; Figure 2; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW32482 standard; Protein; 342
                 93WO-GB00950
                                                 92GB-0009804
92GB-0026928
                                                                                                                                       CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 77.78
Best Local Similarity 82.58
Matches 241; Conservative
                                                                                                                                       Atkinson A, Duggleby
                                                                                                                                                                       WPI; 1993-368798/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 AA;
                                                                                                                                                                                       N-PSDB; AAQ50947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09735887-A1
                 07-MAY-1993;
                                                 07-MAY-1992;
                                                                 24-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1998
                                                                                                                                                                                                                                                           cell walls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW32482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE---KTPEEPKEEVTIKANLIYADGKTQT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG 61
                                                                                                                                                                                                                                                                                                                                                                Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.4%; Score 1226.5; DB 14; Length 1027; 79.9%; Pred. No. 3.2e-84; 1ve 22; Mismatches 31; Indels 9; (
                                                                                                                                                                                                                                                                                                                         Protein L forms a complex with immunoglobulin Kappa light chain. Purified protein can be used as a reagent for immobilising antibodies e.g. on columns, in diagnostic tests and in assays. may also be used in the production of pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide; immunoglobulin; binding; analysis; purification; ELISA; enzyme linked immunoabsorbant assay.
                                                                                                                                                                                                                         for prodn.
                                                                                                                                                                                                                     Immunoglobulin binding polypeptide, protein L - used for pi
of pharmaceuticals and for immobilising antibodies e.g. on
columns, in diagnostic tests and in assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin binding protein derived from protein L.
                                                                                                                                     Duggleby CJ, Murphy JP, Trowern AR;
                                                                                                   (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR42204 standard; Protein; 291 AA
                                                                                                                                                                                                                                                                                           Claim 4; Figure 1; 29pp; English
                                 93WO-GB00949.
                                                                 92GB-0009804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 79.9
Matches 246; Conservative
                                                                                                                                                                     WPI; 1993-368797/46.
                                                                                                                                                                                                                                                                                                                                                                                                               1027 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EQPGE 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 KVDEKPEE 305
                                                                                                                                                                                     P-PSDB; AAR43699
                                                                                                                                     Atkinson A,
                                                                 07-MAY-1992:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-1994
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11-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Query Match
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  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ĥ
                                                                                                                                                                                                                                                       This protein comprises growth factor TLHL, where L is the immunoglobulin binding entity from Peptostreptococcus magnus, H is residues 42-62 of hen eagy lysozyme, and T represents the variable kappa light chain (see AAM91483) from human myeloma protein LEN.

Was expressed in E. coli DH10B cells utilising a DNA construct (see AAP91898) produced from LHL (see AAM91986), kappa (see AAM91990) and synthetic linker oligonucleotides, and was purified from total bacterial lysate via a strep-tag. The linker contains a cleavage is the for tobacco etch virus (TEV) protease. TLHL was designed so that the kappa portion of the protein is cleaved by TEV protease into 'T' and 'LHL' moieties. Production of catalytic antibodies to a specific antigen comprises administering to an animal a growth factor comprising an antigen capable of interacting with a B cell bound catalytic antibody. The antigen is fused to a B cell surface molecule binding protein for the antigen to be cleaved and for the remainder of the molecule to induce B cell mitogenesis (claimed). LHL crosslinks with surface immunoglobulin on B cells. This induces be cell activation and blast formation. Internalisation and processing of LHL leads to the presentation of the H peptide signals the child contains and contains and undergo antibody class switching activated B cell intogralidation and undergo antibody class switching activated B cell intogralidation and undergo antibody class switching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth factor precursor; B-cell surface; T cell surface; CAb; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PKEEVTIKANLIYADGKTQTAEFKGTFE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and secretion. The catalytic antibodies generated by the process can have diagnostic and therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                           New catalytic antibody precursors - comprising a B-cell surface molecule binding portion which can induce B-cell mitogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                         Tarlinton DM, Treutlein HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 618; DB 1
Pred. No. 6e-39;
5; Mismatches
                                                                                                                                                                                                                                  66-68; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06909 standard; Protein; 342 AA.
                                                                                              (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.5%;
75.9%;
                                                                   96AU-0008951.
                           97WO-AU00194
                                                      97AU-0005375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLHL amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKFAGKEKTPEE-----
                                                                                                                         Suess GM,
                                                                                                                                                   WPI; 1997-489572/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 AA;
                                                                                                                                                                                                                                  Example 11; Page
                                                                                                                                                                N-PSDB; AAT91589
                                                                    26-MAR-1996;
                                                                                                                         Koentgen F,
02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY06909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06909
                                                      Db
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The invention relates to a growth factor precursor that comprises B-cell surface binding part, antibody (CAb); and a peptide comprising heavy and light challed antibody (CAb); and a peptide comprising heavy and light chalms of immunoglobulin. When the antigen is cleaved the B cell surface part can interact with its target. The growth factor precursors are used to select B cells that produce Ag-specific CAb, and to generate CAb from such cells (by inducing mitogenesis, caused by the growth factor released by specific cleavage). The Ag-specific CAb can be directed against, e.g. tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock syndrome); viral docking receptors (treatment of human immune virus, hepatitis and influenza infections); tumour-specific antigens; amyloid plaque (treatment of Alzheimer's disease or myeloman) or IGE (treatment of allergies such as asthma). CAD may also be used for drug detoxification, corresponding nucleic acid in a viral or other gene therapy vector. The provet factor or inflammatory diseases and to eliminate environmental or industrial pollutants, such as plastics and perroleum. Particularly the growth factor precursors are produced by delivering the prosent sequence represents the amino acid sequence of TLHL. The LHL is a growth factor comprising H flanked by two L molecules where L is a B cell surface molecule binding portion from protein L of P. magnus; H is a T cell surface molecule binding portion from her egg lysosyme (HEL). TLHL is betting the present sequence to N terminus region.
rheumatoid arthritis; toxic shock syndrome; viral docking receptor; human immune virus; tumour-specific antigen; amyloid plaque; myeloma; Alzheimer's disease; IGE; allergy; asthma; drug detoxification; autoimmune; inflammatory disease; gene therapy; protein L; P. magnus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PKEEVTIKANLIYADGKTQTAEFKGTFE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth factor precursor cleaved by antigen-specific catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treutlein HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.5%; Score 618; DB 20;
75.9%; Pred. No. 6e-39;
tive 5; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 11; Page 67-69; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tarlinton DM,
                                                                                                                                                             hen egg lysosyme; HEL; LHL; TLHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-AU00783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97AU-0009306.
                                                                                                                                                                                                                                    Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koentgen F, Suess GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-244394/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 IKFAGKEKTPEE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX34592
                                                                                                                                                                                                                                                                                                                                                  WO9915563-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .8-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 126;
                                                                                                                                                                                                                                                                           Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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-- PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117

78 FAGKEKTPEE-

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This polypeptide comprises growth factor LHL-omp, where L is the immunoglobulin binding entity from Peptostreptococcus magnus and H is residues 42-62 of hen egg lysozyme. It was generated from LHL.seq (see AAM32481) such that the E. coli ompA signal sequence (generated by purifylng LHL.seq from whole bacterial host cells) was eliminated. The N-terminal omp peptide found in LHL (see AAW32479), LHL.seq (see AAW32481) and TLHL (see AAW32482) induces multimerisation as demonstrated by a potentiation of biological activity as compared to recombinant LHL-omp. Production of catalytic antibodies to a specific antigen comprises administering to an animal a growth factor comprising an antigen capable of interacting with a B cell bound catalytic antibody. The antigen to be cleaved and for the remainder of the molecule to induce B cell mitogenesis (claimed). The observation that omp induces multimerisation allows the design of simpler molecules with the same desired biological function as consistent of the process can have diagnostic and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New catalytic antibody precursors · comprising a B-cell surface molecule binding portion which can induce B-cell mitogenesis
                                                                                                                                                        Catalytic antibody; growth factor; B-cell mitogenesis; LHL-omp;
                                                                                                                        Growth factor LHL-omp (catalytic antibody precursor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treutlein HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tarlinton DM,
                                                                                                                                                                                                                                                                                                /note= "FLAG epitope"
170..178
                                                                                                                                                                                                      Chimeric - Peptostreptococcus magnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 27; Page 76; 109pp; English.
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 /note= "strept-tag"
                             AAW32486 standard; Protein; 178 AA.
                                                                                                                                                                          L protein; hen egg lysozyme; HEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97AU-0005375
                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-AU00194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96AU-0008951
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suess GM,
                                                                                                                                                                                                                     Chimeric - Gallus sp.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-489572/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT91591
                                                                                                                                                                                                                                                                                                                                                                  W09735887-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  applications
                                                                                           27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                02-0CT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                           AAW32486;
                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                  Peptide
RESULT 10
              AAW32486
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The invention relates to a growth factor precursor that comprises B-cell surface binding part, a cell surface binding part, antigen cleavable by a catalytic antibody (CAD); and a peptide comprising heavy and light chains of immunoglobulin. When the antigen is cleaved the B cell surface part can interact with its target. The growth factor precursors are used to select B cells that produce Ag-specific CAD, and to generate CAD from such cells (by inducing mitogenesis, caused by the growth factor released by specific cleavage). The Ag-specific CAD can be directed against, e.g. tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock syndrome); viral docking receptors (treatment of human immune virus, hepatitis and influenza infections); tumour-specific antigens; amyloid plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of alleques stafma). CAD may also be used for drug detoxification, to treat autoimmune or inflammatory diseases and to eliminate environmental or industrial pollutants, such as plastics and petroleum. Particularly the growth factor precursors are produced by delivering the corresponding nucleic acid in a viral or other apene therapy vector. The present sequence represents the amino acid sequence of the LHL growth factor carrying an omph signal peptide (LHL.omp). L is a B cell surface molecule binding portion from her egg lysosyme (HEL). LHL is a growth factor comprising H flanked by two L molecules.
                                                                                                                                                                                                                                                                                                                                                             Growth factor precursor; B-cell surface; T cell surface; CAb; hepatitic catalytic antibody; immunoglobulin; tumour necrosis factor; influenza; rheumatoid arthritis; toxic shock syndrome; viral docking receptor; human immune virus; tumour-specific antique; amyloid plaque; myeloma; Alzheimer's disease; IGB; allergy; asthma; drug detoxification; autoimmune; inflammatory disease; gene therapy; protein L; P. magnus;
72 FAGKEATNRNTDGSTDYGILQINSRWGGLTSAEEVTIKANLIFANGSTQTAEFKGTFEKA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth factor precursor cleaved by antigen-specific catalytic
                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a form of LHL growth factor (LHL.omp).
                                                                118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koentgen F, Suess GM, Tarlinton DM, Treutlein HR;
                                                                                                                                                                                            AAY06913 standard; Protein; 178 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Examples; Page 74; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97AU-0009306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-AU00783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hen egg lysosyme; HEL; LHL.
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-244394/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus sp.
                                                                                                                                                                                                                                    AAY06913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody
                                                                                                                                                   RESULT 11
                                                                                                                                                                     AAY06913
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1;

Score 615; DB 18; Length 178; Pred. No. 4.5e-39; 5; Mismatches 14; Indels 20

39.3%; 76.2%;

Conservative

Matches 125;

12

ογ Dp

Query Match

Similarity

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WPI; 1999-244394/20
                                                                                                  198 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus sp.
                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                  AAY06910;
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody
                                                                                                                                                                                                                                                                            RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin binding entity from Peptostreptococcus magnus and H is residues 42-62 of hen egg lysozyme. It is a modified form of LHL (see AAW32479) having an N-terminal FLAG epitope (see AAW32484) and a C-terminal strep-tag (see AAW32485) that facilitates purification. Production of catalytic antibodies to a specific antigen comprises administering to an animal a growth factor comprising an antigen capable of interacting with a B cell bound catalytic antibody. The antigen is fused to a B cell surface molecule binding protein for
                                                                                                  78 FAGKEKTPEE--------PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117
                                                                                                            Gaps
                                                                       EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises growth factor LHL.seg, where L is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New catalytic antibody precursors - comprising a B-cell surface molecule binding portion which can induce B-cell mitogenesis
                                            20;
                                                                                                                                                                                                                                                                            Catalytic antibody; growth factor; B-cell mitogenesis; LHL.seq; L protein; hen egg lysozyme; HEL.
                        Length 178;
                                            Indels
                                                                                                                                                 118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                           Growth factor LHL.seq (catalytic antibody precursor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tarlinton DM, Treutlein HR;
                         Score 615; DB 20;
Pred. No. 4.5e-39;
                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 70-71; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                           /note= "FLAG epitope"
190..198
                                                                                                                                                                                                                                                                                                        Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
22..29
                                                                                                                                                                                                                                                                                                                                                                                 /note= "strept-tag"
                                                                                                                                                                                                      AAW32481 standard; Protein; 198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATIONS PTY
                         39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96AU-0008951.
                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-AU00194
                                                                                                                                                                                                                                                                                                                                                                                                                                                        97AU-0005375
                                                                                                                                                                                                                                        27-MAR-1998 (first entry)
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suess GM,
                                                                                                                                                                                                                                                                                                                 - Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-489572/45.
                                  Similarity
       178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT91588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMRA-) AMRAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1997
                                          Matches 125;
                                                                                                                                                                                                                                                                                                                 Chimeric
Chimeric
                                                                                                                                                                                                                       AAW32481;
                                                                                                                                                                                                                                                                                                        Chimeric
        Sequence
                          Query Match
                                   Local
                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                      Peptide
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The invention relates to a growth factor precursor that comprises B-cell surface binding part, T cell surface binding part, antigen cleavable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the antigen to be cleaved and for the remainder of the molecule to induce B cell mitogenesis (claimed). LHL.seq has the same biological activity as LHL, which crosslinks with surface immunoglobulin on B cells. This induces B cell activation and blast formation. Internalisation and processing of LHL leads to the presentation of the H peptide on MHC II. T cell recognition of MHC II with the H peptide signals the activated B cell to proliferate and undergo antibody class switching and secretion. The catalytic therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Growth factor precursor cleaved by antigen-specific catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a form of LHL growth factor (LHL.seq).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treutlein HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 615; DB 18;
Pred. No. 5.1e-39;
5; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tarlinton DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 70-71; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY06910 standard; Protein; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.3%;
76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMRA-) AMRAD OPERATIONS PTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-AU00783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAGKEKTPEE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 76.2
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suess GM,
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by a catalytic antibody (CAb); and a peptide comprising heavy and light chains of immunoglobulin. When the antigen is cleaved the B cell surface part can interact with its traget. The growth factor precursors are used to select B cells that produce Ag-specific CAb, and to generate CAb from such cells (by inducing mitogenesis, caused by the growth factor released by specific cleavage). The Ag-specific CAb can be directed against, e.g. tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock syndrome); viral docking receptors (treatment of human immune virus, plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of corresponding nor inflammatory disease and to eliminate convironmental or inflammatory diseases and to eliminate convironmental or inflammatory diseases and to eliminate convironmental or inflammatory diseases and to eliminate corresponding nucleic acid in a viral or other gene therapy vector. The present sequence represents the amino acid sequence of the LHL growth factor acriving a N-terminal FLAG epitope and a C-terminal strep tag. I is a B cell surface molecule binding portion from protein Loft of Pysosyme (HEL). LHL is a growth factor comprising H flanked by two L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 FACKEKTPEE-------PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYANDTLKKDNGEYTVDVADKGYTLNIK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 EEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 615; DB 20; Length 198;
Pred. No. 5.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catalytic antibody; growth factor; B-cell mitogenesis; LHL; L protein; hen egg lysozyme; kappa light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth factor CATAB-TEV (catalytc antibody precursor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treutlein HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tarlinton DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric - Peptostreptococcus magnus.
Chimeric - Gallus sp.
Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW32480 standard; Protein; 495 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 125; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     198 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                     molecules
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
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This polypeptide comprises CATAB-TEV, a synthetic growth factor composed of: (a) TLHL (see AAW91589), where L is the immunoglobulin binding entity of Peptostreptococcus magnus, H is residues 42-62 of hen egg lysozyme, and T represents the variable kappa light chain (see AAW32483) from human myeloma protein LEN; and (b) an additional, C-terminal kappa protein, the elements of CATAB-TEV being joined by linkers containing recognition sites for tobacco etch virus (TEV) protease. CATAB-TEV was designed so that the kappa portions of the protein are removed by TEV protease to release 'T' and 'LHL' comprises administering to an animal a growth factor comprising an antigen capable of interacting with a B cell bound catalytic antibody. The antigen is fused to a B cell surface molecule binding protein for the antigen to be cleaved and for the remainder of the molecule to induce B cell mitogenesis (claimed). LHL (see AAW32479) crosslinks with surface immunoglobulin on B cells. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth factor precursor; B-cell surface; T cell surface; CAb; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalytic antibody; immunoglobulin; tumour necrosis factor; influenza; rheumatoid arthritis; toxic shock syndrome; viral docking receptor; human immune virus; tumour-specific antigen; amyloid plaque; myeloma; Alzheimer's disease; IGE; allergy; asthma; drug detoxification; autoimmune; inflammatory disease; gene therapy; protein L; P. magnus; hen egg lysosyme; HEL; LHL; CATAB-TEV; tobacco etch virus; TLHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 IKFAGKEXTPEE--------PKEEVTIKANLIYADGKTQTAEFKGTFE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   induces B cell activation and blast formation. Internalisation and processing of LHL leads to the presentation of the H peptide on MHC II. T cell recognition of MHC II with the H peptide signals the activated B cell to proliferate and undergo antibody class switching and secretion. The catalytic antibodies generated by the process can have diagnostic and therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
               New catalytic antibody precursors – comprising a B-cell surface molecule binding portion which can induce B-cell mitogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 KATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 614; DB 18;
Pred. No. 1.9e-38;
4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKE 154
                                                                              Claim 12; Page 61-63; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06908 standard; Protein; 495 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATAB-TEV aminoacid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.2%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 125; Conserv
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The invention relates to a growth factor precursor that comprises B-cell surface binding part, antigen cleavable by a catalytic antibody (CAB); and a peptide comprising heavy and light chains of immunoglobulin. When the antigen is cleaved the B cell surface part can interact with its target. The growth factor precursors are used to select B cells that produce Ag-specific CAB, and to generate CAB from such cells (by inducing mitogenesis, caused by the growth factor released by specific cleavage). The Ag-specific CAB can be directed against, e.g. tumour necrosis factor (treatment of rheumatonia arthritis or toxic shock syndrome); viral docking receptors (treatment of human immune virus, hepatitis and influenza infections); tumour-specific antigens; amyloid plaque (treatment of Alzhaimer's disease or myeloma) or IGE (treatment of plaque (treatment of Alzhaimer's disease or myeloma) or IGE (treatment of alleryies such as asthma). CAB may also be used for drug detoxification, to treat autoimmune or inflammatory diseases and to eliminate environmental or industrial pollutants, such as plastics and petroleum. Particularly the growth factor precursors are produced by delivering the corresponding nucleic acid in a viral or other gene therapy vector. The particularly the growth factor precursors are produced by delivering the is assembled from Till and kappa by PCR. The LHL is a growth factor comprising H flanked by two L molecules where L is a B cell surface molecule binding portion from hen egg lysosyme (HEL). TLHL is LHL linked to kappa chain via TBY (tobacco etch virus) sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth factor precursor cleaved by antigen-specific catalytic
                                                                                                                                       Koentgen F, Suess GM, Tarlinton DM, Treutlein HR;
                                                                                                                                                                                                                                                                                                                          Example 15; Page 64-66; 101pp; English.
                                                                                         (AMRA-) AMRAD OPERATIONS PTY LTD.
                                             97AU-0009306.
98WO-AU00783
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Matches 125; Conservative
                                                                                                                                                                                     WPI; 1999-244394/20.
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18-SEP-1998;
                                             19-SEP-1997;
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Search completed: October 29, 2002, 09:29:25 Job time : 25.9378 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein . protein search, using sw model

October 29, 2002, 09:25:26; search time 10.571 Seconds (without alignments) 1589.653 Million cell updates/sec Run on:

US-08-325-278B-3 2235 Title: Perfect score: Sequence:

1 AVENKEETPETPETDSEEEV.......GVDGVWTYDDATKTFTVTEM 434 Scoring table:

105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P19909 streptococc P06654 streptococc Q53554 stephylococc P07197 homo sapien P20075 daucus caro P80644 staphylococ P16397 baccillus su P43597 saccharomyc P39653 streptococc Q07833 bacillus su P08533 mus musculu P49051 bacillus an P12839 rattus norv P12839 rattus norv P15205 rattus norv P15205 rattus norv P16925 rattus norv P16925 streptococc P02565 gallus gall P16939 cyprinus ca O77788 bos traurus P5516 salmonella Q0339 dictysosteli P16738 staphylococc P03690 dictysosteli P16739 staphylococc P03690 dictysosteli P1338 staphylococc P03690 saccharomyc P1313 dlostridium Q03690 saccharomyc P18837 bacillus sp	1
SUMMARIES DB ID	SPG2_STRSP SPG1_STRSP CNA_STRAU INFM_HUMAN EDC8_DAUCA MRSP_STAAU ABP2_HUMAN YF16_YEAST ABP2_HUMAN YF16_YEAST MAPA_BACSU NFM_MOUSE NFM_MOUSE NFM_BAT MAPB_RAT MAPB_RAT MAPB_RAT MAPB_RAT MAPB_RAT MAPB_RAT MAPB_RAT MAPB_RAT MAPB_RAT MYSS_CYPCA NFW_SC_CYPCA NFW_SC_C	A
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Result No.		

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SLPW_BACBR NFM_RABIT SA30_PLAFFO CWBA_BACSU NUCL_MOUSE CSG_HALHA SLPH_BACBR P1P_LACLC CA1C_HUAN HIBN_XENLA EAE_ECO57
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ALIGNMENTS

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RESULT SPG2_S ID S	RESULT 1 SPG2_STRSP STANDARD; PRT; 593 AA.
AC	
55	(Rel. 17,
1 E	15-JUL-1999 (Rel. 38, Last annotation update)
DE	in G binding pr
S	SPEC
8 O	Streptococcus sp. (strain 6148). Bacteria: Firmicutes: Bacillus/Clostridium group: Streptococoaceae:
88	
χo	NCBI_TaxID=1306;
RN	[1]
A P	SEQUENCE FOR N.A.
X	SIKAIN-0140; MEDLINE-88029445; PubMed-3665928;
RA	Olsson A., Eliasson M., Guss B., Nilsson B., Hellman U.,
RA	Lindberg M., Uhlen M.;
RT	"structure and evolution of the repetitive gene encoding
Z.	tococcal protein G.
Z Z	Eur. J. BIOCNEW. 108:319-324(198/).
90	(2) CROITENCE FROM N A
2	STRAIN STANDS
X	MEDI.TNE#88015586: PubMed#365869:
RA RA	Filbula D., Alexander P., Fahnestock S.R.;
RT	"Nucleotide sequence of the protein G aene from Streptococcus GX7805,
RT	and comparison to previously reported sequences.";
RL	Nucleic Acids Res 15:7210-7210(1987).
RN	[3]
RP	SEQUENCE OF 114-593 FROM N.A.
RC S	STRAIN=G148;
RX	
RA	Guss B., Eliasson M., Olsson A., Uhlen M., Frej AK., Joernvall H.,
RA	
· RT	"Structure of the IgG-binding regions of streptococcal protein G.";
RL	EMBO J. 5:1567-1575(1986).
RN	[4]
RP	STRUCTURE BY NMR OF 371-427.
אן בי	STKAIN=G148;
XX.	MEDLINE=88290449; PubMed=9628485;
X E	
Y E	"Design, structure and stability of a hyperthermophilic protein
I I	Validit; Nat chruck Diol 6.470.478/1000.
5	Nat. Stiucti Digit - 3.470 470 470 470 470 470 470 470 470 470
200	- I - SIMILARITY: TO OTHER STREPTOCOCCAL AND STADHYLOCOCCAL DROTTINS
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ပ္ပ	This SWISS-PROT entry is copyright. It is produced through a collaboration
ပ္ပ	between the Swiss Institute of Bioinformatics and the EMBL outstation -
ပ္ပ	the European Bioinformatics Institute. There are no restrictions on its
2 8	non-profit institutions as long as its con
3 8	and this statement is not removed.
ر د	entities requires a license agreement (see http://www.isb-sib.ch/announce/

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PIR; A24496; A24496.
PDB; 1PGA; 30-APR-94.
PDB; 1PGB; 30-APR-94.
PDB; 1PGX; 15-JUL-92.
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P06654;
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                                   HID DAY NEW TRANKER TO THE TOTAL TO THE TOTA
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                                                                           PIR; A26314; A26314.

R PIR; A26314; A26314.

R PDB; IGB4, 22-UL-98.

R InterPro; IPR002989; Gram_pos_anchor.

R InterPro; IPR001899; Gram_pos_anchor.

R InterPro; IPR001899; Gram_pos_anchor.

R Pfam; PF01468; Gram_pos_anchor; 1.

R Pfam; PF01378; IgG_binding_B; 3.

R Pfam; PF01378; IgG_binding_B; 3.

R PRIMYS; PR00015; GPOSANCHOR.

R PROSITE; PS00343; GRAM_POS_ANCHORING; 1.

R IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KTQTAEFKGTFEEATAEAYRYADALKKDNGE---YTVDVADKGYTLNIKFAGKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 LSDFLKSQTP-----AEDTVKSIELAEAKVLANRELDKYGVSDYHKNLINNAKTVEGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YTVDVADKGYTLNIK - FAGKEKTPEE - - - - - PKEEVTIKANLIYADGKTQTAEFKGTFAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 TPEEPKEEVTIKANLIYA-DG-----KTQTAEFKGTFEEATAEAYRYAD---LLAKENGK
                                                                                                                                                                                                                                                                                                                   IMMUNOGLOBULIN G BINDING PROTEIN EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 X 5 AA REPEATS OF [DE]-D-A-K-K. CONSERVED IN GRAM-POSITIVE COCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.7%; Score 708; DB 1; Length 593; 48.3%; Pred. No. 1.2e-31; ive 28; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             048BAA760D5B2920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                        37 AA REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA REPEATS
or send an email to license@isb-sib.ch)
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                            EMBL; X06173; CAA29540.1; -. EMBL; Y00428; CAA68489.1; -. EMBL; X04015; CAA27638.1; -.
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Matches 205; Conserv
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568
568
589
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VTEM 498
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Immunoglobulin G binding protein G precursor (IGG binding protein G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS) OF 292-352.
Butterworth S., Lamzin V.S., Wigley D.B., Derrick J.P., Wilson K.S.; Submitted (APR-1997) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
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MEDLINE=95308043; PubMed=7788293;
Sauer-Eriksson A.E., Kleyweqt G.J., Uhlen M., Jones T.A.;
Crystal structure of the C2 fragment of streptococcal protein G in complex with the Fc domain of human 196.";
                                                                                                                                                                                                                                                        Streptococcus sp. (Lancefield group G).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
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MEDLINE=91335209; PubMed=1871600;
Gronenborn A.M., Filpula D.R., Essig N.Z., Achari A., Whitlow M., Wingfield P.T., Clore G.M.;
"A novel, highly stable fold of the immunoglobulin binding domain streptococcal protein G.";
Science 253:657-661(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallagher T., Alexander P., Bryan P., Gilliland G.L.; "Two crystal structures of the Bl Immunoglobulin-binding domain streptococcal protein G and comparison with NMR."; Biochemistry 33:4721-4729(1994).
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of the structure alone and in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fahnestock S.R., Alexander P., Nagle J., Filpula D.; "Gene for an immunoglobulin-binding protein from a group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS) OF 228-282
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448 AA
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Derrick J.P., Wigley D.B.;
"The third IgG-binding domain from analysis by X-ray crystallography ocomplex with Fab.";
J. Mol. Biol. 243:906-918(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86304178; PubMed=3745123; Fahnestock S.R., Alexander P., Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94213848; PubMed-8161530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 167:870-880(1986).
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 streptococcus.
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01-JAN-1988 (
16-OCT-2001 (
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NCBI_TaxID=1280;
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Best Local Simi
Matches 136;
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CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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                                                                                                                                                                                                                                                                                    IMMUNOGLOBULIN G BINDING PROTEIN G.
                                                                                                                                                        Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF01378; IgG_binding_B; 2.
PRINTS; PR00015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
IgG-binding protein; Repeat; Transmembrane; Cell wall; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.6%; Score 683; DB 1; Length 448; 53.2%; Pred. No. 1.9e-30; Live 15; Mismatches 92; Indels
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
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2 x 37 AP
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InterPro; IPR01899; Gram_pos_anchor.
InterPro; IPR001809; IgG_bind_B.
Pfam; PF01468; GA; 2.
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nes 176; Conservative
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             01-NOV-94.
29-JUL-98.
20-JUL-95.
15-APR-93.
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15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 X 187 AA APPROXIMATE TANDEM REPEATS.
LYS/PRO-RICH (CELL WALL-SPANNING).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patti J.M., Boles J.O., Hoeoek M.;
"Identification and biochemical characterization of the ligand
binding domain of the collagen adhesin from Staphylococcus aureus.";
Biochemistry 32:11428-11435(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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-!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                          æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Narayana S.V.L.; "Structure of the collagen-binding domain from a Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1183;
                                                                                                       Lindberg M., Hoeoek M.; "Molecular characterization and expression of a gene encoding Staphylococcus aureus collagen adhesin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Teale M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Struct. Biol. 4:833-838(1997).
                                                                             Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,
                                                                                                                                                                                                                                                                               Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
MEMBRANE ARCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
COLLAGEN-BINDING.
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PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
Signal; Repeat; Transmembrane; Cell wall; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Symersky J., Patti J.M., Carson M., House-Pompeo K.,
Moore D., Jin L., Schneider A., DeLucas L.J., Hoeoek
Narayana S.V.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.4%; Score 188.5; DB 1;
23.8%; Pred. No. 0.0032;
live 61; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 169-318.
MEDLINE=97475225; PubMed=9334749;
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                                                                                                                                                                                                                                                                                                      Lindberg M., Hoeoek M.;
J. Biol. Chem. 269:11672-11672(1994)
                                                                                                                                                                                        Biol. Chem. 267:4766-4772(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLAGEN-CONTAINING SUBSTRATA.
                         STRAIN-FDA 574;
MEDLINE-92165839; PubMed-1311320;
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94032261; PubMed-8218209;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
         OF AXONAL CALIBER.
PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LEAGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHARGE IN THE NEUROFILAMENT FUNCTION.
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 KEEVTIKANLIYADGKTQTAEF------KGTFAEATAEAYRYADLLAKENGKYTA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 DLEDGGYTINIRFAGK--KVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVF-- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------VDGEWTYDDATK- 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       758 KETKEEGKPLQOEKEKEKAGGEGGSEEEGSDKGAKGSRKEDIAVNGEVEGKEEVEQETKE 817
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LINKER 2.
COIL 2B.
6 X 13 AA TANDEM REPEATS.
6 - LINKED (GLCNAC) (BY SIMILARITY).
6 - LINKED (GLCNAC) (BY SIMILARITY).
MW; 5F5D3DF34C9D9E50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 156; DB 1; Length 915;
Pred. No. 0.13;
5; Mismatches 153; Indels 172;
                                                                                                                                                                                                                                                                                               Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                     HEAD.
ROD.
TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
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4 411
2 915
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247
264
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102317 M
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Matches 117; Conservative
                                                                                                                                                                                                                  PIR; A27864; A27864
PIR; A30157; A30157
MIM; 162250; -.
                                                                                                                                                                                                                                                                                                                                                 104
412
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INIT_MET
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        864
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
NCBI_TaxID=4039;
--TFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNG
                       X APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.9%; Score 155; DB 1; Length 555; 33.9%; Pred. No. 0.083;
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                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Embryonic protein DC-8 (Clone 8/10).
                                                                                                                                                                                                                        555 AA.
                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV. QUEEN ANNE'S LACE;
MEDLINE-89384429; PubMed-2571069;
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                                                                              VDGVWTYDDATKTFTVTE 433
                                                                                                                    GDGATKY -- ITKSVTVTQ 880
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                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  Daucus carota (Carrot).
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281
303
325
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InterPro; IPR004238;
Pfam; PF02987; LEA; 6
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P20075;
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18;

Gaps

:96

57; Mismatches 187; Indels

23.9%;

Best Local Similarity 23.9 Matches 107; Conservative

Query Match

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                                                                                                                                                87 DYAYDKGREGGDVAAQKAEEAKEKAKMAKDTTMGKAGEYKDYTAQKA-----EEAKEKA 140
                                                                                                                                                                                                  122 YRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKT---PEEPKEEVTIKANLIYADGKTQ 178
                                                                                                                                                                                                                                                                                                                                                  191 TAOKAAEAKEKTGE---YKDYAAOKAAEAKVLAAQKA-----AEAKDTTGKDGEYKDYA 241
                                                                                              EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
61
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STRAIN-ISOLATE 1061;
Savolainen K., Kuusela P., Paulin L., Korhonen T.K.;
"Pls, a large repeat-rich surface protein of methicillin resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                   141 AQKAEETKEKAGEY-----KNYTAQKAGEAKDTTLGKAGEYKDYAAQKA----AEAKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 OKTGEYKDYSAQKAAETKDATMEKTKEYKDYTAQKAAETKDATMEKAKEAKDTTVQKTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 FKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTK
2 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG
                                               40 VEHKEEVSGGPG-----VIGSILKSVQGTLGQAK-----EVVVGKAHDTAE-VSRENT
                                                                                                                                                                                                                                                                                                   179 TAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE--EPKEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFAGKKVDEKPEEPMDTYKLIL-NGKTLKGETTTEAVDA--ATAEKV------
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Hilden P., Savolainen K., Tyynelae J., Vuento M., Kuusela P.;
"Purification and characterisation of a plasmin-sensitive surface
protein of Staphylococcus aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                      237 TIKANLIYADGK----TQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    676-682; 938-948; 1156-1168; 1176-1185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBL_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Methicillin-resistant surface protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1637 AA.
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STRAIN=168;
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                                  Pero
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 17;
         Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
Cell wall; Transmembrane; Antibiotic resistance; Glycoprotein; Repeat;
                                                             METHICILLIN-RESISTANT SURFACE PROTEIN.

141 X 2 AA TANDEM REPEATS OF D-[SAG].

CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (Rel. 15, Created)
01-FBE-1996 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Bacillopeptidase F precursor (EC 3.4.21.-) (Esterase) (RP-I protease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sloma A., Rufo G.A. Jr., Rudolph C.F., Sullivan B.J., Theriault K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Bacillopeptidase F of Bacillus subtilis: purification of the protein
                                                                                                                                                  Indels 109; Gaps
                                                                                                                                                                       62
                                                                                                                                                                       ENKEETPETPETPETBSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE
                                                                                                                                                                                                                 63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY
                                                                                                                                                                                                                                                        123 RYADALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYA----D
                                                                                                                                                                                                                                                                            171 K------TEETDKATTEEAPAAEETSKAATEEAPKAEETSKAATEEAPKAEET
                                                                                                                                                                                                                                                                                                 175 GKTQTAEFKGTFEE---ATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEE
                                                                                                                                                                                                                                                                                                                      218 EKTATEEAPKTEETDKVETEEAPK----AEETSKAATEKAPKAEETN----KVETEEA
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                                                                                                                                                                                                                                                                                                                                                         287 GYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGV
                                                                                                                                                                                                                                                                                                                                                                                                  Length 1637;
                                                                                                       75BE9ADB469BD309 CRC64;
                                                                                                                                        ; Pred. No. 0.46;
34; Mismatches 200;
                                                                                                                              DB 1;
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                                                                                                                                      0.46;
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SEQUENCE FROM N.A., AND SEQUENCE OF 195-222.
MEDLINE-90170864; Pubmed-2106512;
MEDLINE-90170864. Sulli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AFKQYANDN-GVDGVWTYDDA---TKTFTVT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 TLTAFNTNFNPNTGTKGALEYNDKIDFNKDFTIT 455
                                                                                                                             Query Match 6.8%; Score 151.5; Best Local Similarity 24.4%; Pred. No. 0.4 Matches 111; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1423;
                                                     POTENTIAL.
                                                                                               PROTEINS
InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cloning of the gene.";
Bacteriol. 172:1470-1477(1990)
                                                                                                          MM.
                                                                                                       1637 AA; 174573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (90 kDa serine proteinase)
BPR OR BPF.
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1603
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16-OCT-2001 (
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ID SUBF_BACSU
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REVISIONS.
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                              Sullivan B.J., Theriault K.A.,
                                                                                                                                                                                                           Wu X.-C., Nathoo S., Pang A.S.-H., Carne T., Wang S.-L.; "Cloning, genetic organization, and characterization of a structural gene encoding bacillopeptidase From Bacillus subtilis."; J. Biol. Chem. 265:6845-6850(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y.;
Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kato T., Yamagata Y., Arai T., Ichishima E.;
"Purification of a new extracellular 90-kDa serine proteinase with
"soelectric point of 3.9 from Bacillus subtilis (natto) and
elucidation of its distinct mode of action.";
Biosci. Biotechnol. Biochem. 56:1166-1168(1992).
-: SUBCELLULAR LOCATION: Secreted.
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masuda E.S., Anaguchi H., Sato T., Takeuchi M., Kobayashi "Nucleotide sequence of the sporulation gene spoilGA from subtilis.";
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CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-211 FROM N.A.
MEDLINE=89008108; PubMed=3139638;
Beall B., Lowe M., Lutkenhaus J.;
"Cloning and characterization of Bacillus subtilis B. Escherichia coli cell division genes ftsz and ftsA."
J. Bacteriol. 170:4855-4864(1988).
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InterPro; IPR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 1.
PROTO723; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_ASP; FALSE_NEG.
PROSITE; PS00136; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_HIS; 1.
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                        Sloma A., Rufo G.A. Jr., Rudolph C.F.,
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                                                                                      Bacteriol. 172:5520-5521(1990).
                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=90216713; PubMed=2108961;
MEDLINE=90368623; PubMed=2118514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M29035; AAA62679.1; -.
EMBL; J05400; AAA83362.1; -.
EMBL; M22630; AAA22458.1; -.
EMBL; X1344; CAA35224.1; -.
EMBL; Z99111; CAB13403.1; -.
EMBL; Z99112; CAB13404.1; -.
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A36734; A36734.
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MEROPS: S08.017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAAVPEITSPIDKSYINKDSVTVKGNA-----SPGTTVHIYNGEKEAGETKAAADGTF 1205
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                                                                                                                                                                                                                                                                                                                            61 GEYTVDVADKGYTLNIKFAGKEKTPE-EPKEEVTIKANLIYADGKTQTAEFKGTFEEAT- 118
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                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                2 VENKEETPETPETPESEEEVTIKANLIFANGSTQTAEF-KGTFEKATSEAYAYADTLKKDN 60
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                                                                                                                                                                                                                                                                                   815 VNPKKAKPSANTAVKHONKALOPOVLPLKAQVSVVETGKSTYSDQSTGQY----TLKHKA
                                                                                                                                                                                                                                                                                                                                                                    871 GDYTLMAEAYGY-----QSKTQKVSLKTDQTTQANFTLEEMKKGT--LKGTVINKTT
                                                                                                                                                                                                                                                                                                                                                                                                            119 ----AEAYRYAD----ALKKDNGEYTVDVADKGYTLNIKFAG--KEKTPEEPKEEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EFKGTFEEAT------AEAYRYADLLAKENGKYT-VDVADKG-
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
T -> A (IN REF. 6).
A -> V (IN REF. 3).
KPQMAA -> N (IN REF. 3).
OPQVLP -> RTRLYS (IN REF. 3).
AQVSVVETG -> FCRSRHKSV (IN REF. 3).
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01-MAY-1991 (Rel. 18, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Endothelial actin-binding protein (ABP-280) (Nonmuscle filamin)
FLNI OR FLN.
                                                                                                                                                                                                        59; Mismatches 187; Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-905361737; Pubbed=2931361;
GOTLIN J.B., Yamin R., Egan S., Stewart M., Stossel T.P.,
Kwiatkowski D.J., Hartwig J.H.;
"Human endothelial actin-binding protein (ABP-280, nonmuscle
filamin): a molecular leaf spring.";
J. Cell Biol. 111:1089-1105(1990).
                                                                                                                                                                6.7%; Score 149; DB 1; Length 1433; 11.6%; Pred. No. 0.54;
                                                                                                     33 MISSING (IN REF. 3).
154577 MW; 98DF6846897807C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IKANLIYADGKTOTA------
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                                                                                                                                                                                   21.6%;
                                                                                                                                                                                                          Matches 116; Conservative
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SEQUENCE FROM N.A.
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P21333;
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                                                                                                                        SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               *Mapping of two genes encoding isoforms of the actin binding protein ABP-280, a dystrophin like protein, to Xq28 and to chromosome 7."; Hum. Mol. Genet. 2:761-766(1993).

-1- FUNCTION: PROMOTES ORTHOGONAL BRANCHING OF ACTIN FILAMENTS AND LINKS ACTIN FILAMENTS TO MEMBRANE GLYCOPROFINS.

-1- SUBCLIDIAR LOCATION: PERIPHERAL CYTOPLASM.
-1- SUBCLIDIAR LOCATION: PERIPHERAL CYTOPLASM.
-1- TISSUE SPECIFICITY: UBIQUITOUS.
-1- TISSUE SPECIFICITY: UBIQUITOUS.
-1- PTM: PHOSPHORYLATION EXTENT CHANGES IN RESPONSE TO CELL ACTIVATION.
                                                                                                                                "Long-range sequence analysis in Xq28: thirteen known and six candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and
MEDLINE=96311563; PubMed=8733135;
Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.-N.,
Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D.,
D'Urso M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN WA ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FODRIN).
-:- SIMILARITY: CONFAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
-:- SIMILARITY: CONTAINS 24 FILAMIN REPEATS.
                                                                                                                                                                                                                                                                                                    MEDIINE-93357748; PubMed-7689011;
Maestrini E., Patrosso C., Mancini M., Rivella S., Rocchi M.,
Repetto M., Villa A., Frattini A., Zoppe M., Vezzoni P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIN-BINDING (HEAD).
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FILAMIN 2.
FILAMIN 3.
FILAMIN 4.
FILAMIN 6.
FILAMIN 6.
FILAMIN 7.
FILAMIN 9.
FILAMIN 9.
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PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; 1.
PROSITE; PS50021; CH; 2.
ACTIN-binding; Phosphorylation; Repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001589; Actinin_act_}
Interpro; IPR001715; Calponin_hom
Interpro; IPR001298; Filamin.
                                                                                                                                                                                                                   Hum. Mol. Genet. 5:659-668(1996)
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SEQUENCE OF 1658-1772 FROM N.A.
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EMBL; L44140; AAA92641; --
EMBL; X70082; CAA49697.1; --
EMBL; X70085; CAA49690.1; --
EMBL; X37098; A37098.
HSSP; P13466; IKSR.
MIM; 300017; --
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Pfam; PF00630; Filamin; 24.
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Streptococcus downei (Streptococcus sobrinus).
                    SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
MEDLINE=95400292; Pubmed=7670463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEAYAYADTLKKDNGEYTVDVADKG---YTLNIKFAGKEKTPEEP---KEEVTIKANLIY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818 AEADIDFDIIRNDNDTFTVKYTPRGAGSYTIMVLFA-DQATPTSPIRVKVEPSHDASKVK 876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 TL-NIKFAGKEKTPEEPKEEVTIKANLIYADG-----KTQTAEFKGTFAEA---TA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2647;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 137.7 kDa protein in UGSI-FAB1 intergenic region.
FFR016C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : : | | : : | | 1.1285 ITQTGGPHVKARVANPSGNLTETYVQDRG-DGMYKVEYTPYEEGLHSVDVT 1334
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                                                                                                                                                                                                                                                                                             SELF-ASSOCIATION SITE, TAIL. CLEAVAGE (BY CALPAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                      6C1A07041DFA3D42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 6.6%; Score 148.5; DB 1;
Best Local Similarity 21.8%; Pred. No. 1.2;
Matches 116; Conservative 66; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                     -> G (IN REF. 3)
-> D (IN REF. 2)
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                            HINGE 1.
FILLAMIN 16.
FILLAMIN 17.
FILLAMIN 19.
FILLAMIN 20.
FILLAMIN 21.
FILLAMIN 21.
FILLAMIN 22.
HINGE 2.
                                                                                                                                                                                                                                                                   FILAMIN 24.
FILAMIN 15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPEEPMDTYKLILN 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD-GKTQTAEFKGT---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      525 AGEKSSIIEIEGSANSAKIS-------KDNLVLEDEAEAPTQENKPTEVVGE 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 --FEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 YADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          674 PKVVKRCTSGRPEDLQINERDPEVLKEDVRVPDEDVKPEIATTIENSEEEDPKSQRVQIS 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           768 GDKITGKDTNHEHGEATEAASENSKASDVGTAEKYIEPSSESVKKDTEEDAEVENSEKTE 827
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                                                                                                                                                    Sacchāromyces cerevisiae.";
Nat. Genet. 10:261-268(1995).
-!- SIMILARITY: SOME, TO MAMMALIAN NEUROFILAMENT TRIPLET M PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-1., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K., Yamazaki M., Tashiro H., Eki T.; "Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.6%; Score 148; DB 1; Length 1233;
21.2%; Pred. No. 0.51;
rative 64; Mismatches 181; Indels 124;
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-glucanohydrolase).
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WAPA OR N17G.
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                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                          EXTRACELLULAR (BY SIMILARITY).

REMBRANE ANCHOR (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 DNGEYTVDV-ADK-----GYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKG 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----YKFSKHLK-----AGEGYKMQ---SGDLKIPASQFENNHGYLLKVR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 LIYADGKTQTAEFKGTFEEATAEAY-RYA------DLLAKENGKYTVDVAD-KGYT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 VRDADNNTLSEVNKAIAVESDWTKFPRYGIVGGSQDTNNSLLSKDADRYRAEIEKMKNMN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --EATAEAYRYADLL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 EQTP--PETSDASAPATTSADSVEKYAODATONOSSTSNGPGVIRATSAOVTATRSVVSS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EETPETPET-DSEEEVTIKANLI--FANGSTQ----TARFKGTFEKATSEAYAYADTLKK 58
        Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 146.5; DB 1; Length 1337; .
; Pred. No. 0.68;
64; Mismatches 181; Indels 171; (
                                                                                                                                                                                                                                                                                                EMBL; M96978; AAA21772.1; -.
InterPro; IPR001899; Gram_pos_anchor.
Pfam: PF00746; Gram_pos_anchor. 1.
PROSITE; PS00343; GRAM POS_ANCHORING; 1.
Hydrolase; Glycosidase; Signal; Transmembrane; Repeat; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                            B494275A77A2E3D0 CRC64;
                                            31-36
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                                           FROM N.A., AND SEQUENCE OF 15 / UAB66;
                                                                                                                                                                                                                                                                                                                                                                                                            1337 AA; 143298 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 20.9°
Matches 110; Conservative
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                          NCBI_TaxID=1317;
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                 Streptococcus
                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE IDL AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED MOTIF REPRATED 31 TIMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
369 ILAE-NTNTGEAPVLPETEYAYNSDDRGYGAQGQPMSYTVKIPKDGQEEDVEIQRYYNPT 427
                                                                                          AKENGKYTAD-----LEDGGY-----TINIRFAGKKVDEKPEEPMDTYKLILNGKTLKG 321
                                                                                                                                                                                                                                                                                                                                              479 ---TEGYAEFLRAIKEKLPNYYLTVNDVNGEQIYRLKDGNQDVIYNEIWPFGPALPSEMA 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95219088; PubMed-7704263;
Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
Cloning and sequencing of a 29 kb region of the Bacillus subtilis
genome containing the hut and wapA loci.";
Microbiology 141:337-343(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168 / BGSC1A1;
MEDLINE=97124196; PubMed=8969509;
Voshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
Miwa Y., Fujita Y.;
"Sequencing of a 65 kb region of the Bacillus subtilis genome
containing the lic and cel loci, and creation of a 177 kb contig
covering the gnt-sacXr region.";
Microbiology 142:3113-3123(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular analysis of three major wall-associated proteins of
Bacillus subtilis 168: evidence for processing of the product of
gene encoding a 258 kDa precursor two-domain ligand-binding
                                                                                                                                                                           428 SKLWQDYIADKMGQAMKNGGFDGWQGDTIGDNEVYSYADKDSNDPSKKFWL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                        362 TEKPEVIDASELTPAVT -- TYKLVINGKTLKG-ETTTKAVDAETAE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              536 AVKPNTVTSRPVLTKVRQGDWKISIVGAYMEGSENGGSKADAEAGK 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2334 AA
                                                                                                                                                                                                                                                                 322 ETTTEAVD---AATAEKVFKQYANDNGVDGE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wall-associated protein precursor
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203 ENGKYTVDVADKGYTLNIKFAGKEKTPE------EPKEEVTIKA-NLIYADGK-- 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1591 SATGTVWFDDIRLIEGSLLTKSTYDSNGNYVTKEEDELGYATSTDYDETGKKTSETDAKG 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1651 ---EKTTYTYDQADQLTNMTLSNGTSILHSYDKEGNEVSKTIRAGADQTYKFEYDVMGKL 1707
                                                                                                                                                                                                                                                                       31 X 21 AA APPROXIMATE TANDEM REPEATS OF X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 GYTLNIKF------AGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 TFEEATAEAYRYADAL-------KKDNGEYTVDV---ADKGYTLNIKFAGKE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                      OR 32 (POTENTIAL).
WALL-ASSOCIATED PROTEIN.
3 X 101 AA APPROXIMATE TANDEM REPEATS.
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                                                                                                                                                                  Repeat; Signal; Complete proteome
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 send an email to license@isb-sib.ch)
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                                         D31856; BAA06656.1; -. D29985; BAA06260.1; -. D83026; BAA11683.1; -. Z99124; CAB15959.1; -.
                             EMBL; L05634; AAA22883.1; -.
                                                                                                   PIR; 532920; 532920.
SubtiList; BG10797; wapA.
InterPro; IPR003305; CBD_6.
Pfam; PF02018; CBD_6; 1.
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Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF AXONAL CALIBER.

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                  1827 NQFTYNKLDQMIEMKDSTSSYSFDYDENGNVQTFITGNGGGTSFSYDERNLVSSLHIGDK 1886
                                                                                                                                                                                                                                                                                                          NGNETSVVNKEQNTTKKRTFDNKNRLTELTDRGGSQTWTYPSDSDKLKTFSWIHGDQKGT 1826
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                                                                                          -----TQTAEFKGTFAE-----E 275
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                                                                                                                                                                                                                                                 NG-----KYTADLEDGGYTINIRFAGK-----KVDEKPEEPMD-----TYKLILNG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] SEQUENCE FROM N.A. MEDMED-1036526; MEDITINE-87246694; PubMed-3036526; Levy E., Liem R.K.H., D'Eustachio P., Cowan N.J.; "Structure and evolutionary origin of the gene encoding mouse NF-M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Julien J.-P., Meyer D., Flavell D., Hurst J., Grosveld F.; "Cloning and developmental expression of the murine neurofilament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
M protein (160 kDa neurofilament protein)
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SEQUENCE OF 322-540 FROM N.A.
MEDLINE-87158637; PubMed=3103856;
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P08553; O61961;
O1-AUG-1988 (Rel. 08, Created)
01-NOV-1990 (Rel. 16, Last sequ
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene family.";
Brain Res. 387:243-250(1986).
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
S-layer protein sap precursor (Surface layer protein) (Surface array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518 KEEEEEGQEEEEEEDEGVKSDQAEEGGS----EKEGSSEKDEGEQEEEEGTEAEGEGEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.4%; Score 143.5; DB 1; Length 848; 22.9%; Pred. No. 0.57; tive 53; Mismatches 151; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
SIMILARITY)
                                                                                      InterPro; IPR001664; IF.
Pfam; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
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5F251F274D0F13B6 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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LINKER 2.
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COIL 1A.
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             EMBL; X05640; CAA29127.1; -. EMBL; M20481; AAA39815.1; -. PIR: S00030; S00030. MGD; MGI:97314; Nfm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 22.9991; Conservative
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INIT_MET
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 DKVLVKEVTLSEDKKSATVELYSNLAAKQTYTVDVNKVGKTEVAVGSLEAKTIEMADQTV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 GKVVAESK-EVKVSAEGAAVASISNWTVAEQNKADFTSKDFKONNKVYEGDNAYVQVELK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQFNAVITGKVEYESLNTEVAVVDKATGKVTVLSAGKAPVKVTVKDSKGKELVSKTVEIE 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 FAEAT-----AEAYRYADLLAKENG----KYTADLE---DGGYT-INIRFAGK 297
                                                                                                                                      MEDITINE—95138020; PubMed—7836294;
Etienne-Toumelin I., Sirard J., Duflot E., Mock M., Fouet A.;
"Characterization of the Bacilius anthracis S-layer: cloning and
sequencing of the structural gene.";
J. Bacteriol. 177:614-620(1995).
-!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SUPERCE OF BACTERIA.
-!- SUBCELLULAR LOCATION: Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YADGKTQ---TAEFKGTFEEATAEAYRY-ADALKKDNGEYTVDVADKGYTLNIKFAGKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KTPEEPKEEVTIKA-------NLIY-ADGKTOTAEFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVENKEETPETPETDSEEVTIKANLIFANGSTQTAE--FKGTFEKATSEAYAYAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TLKKDNGEYTVDV----ADKGYTLNIKFAGKEKTPEEPKEEVTIKA--NLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GTFEEATAEAYRYADL-----LAKENGKYTVDVADKG-YTLNIKFA-GKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KTPEEPKEEVT------EFKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 AFAQKAMKEIKLEKTNVALSTKDVTDLKVKAPVLDQYGKEFTAPVTVKVLDKDGKELKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVDEKPEE------PMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNG
                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 30-40; 209-218; 281-291 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 814;
                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: PROBABLY GLYCOSYLATED.
-!- SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; Cell wall; S-layer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 142.5; DB 1;
22.5%; Pred. No. 0.62;
tive 59; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-LAYER PROTEIN SAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 236946; CAA85408.1; -. InterPro; IPR003343; Big_2. InterPro; IPR001119; SLH. Pffam; PF02368; Big_2; 1. Pffam; PF00395; SLH; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Glycoprotein; SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    814 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 129; Conserv
NCBI_TaxID=1392;
                                                                                                                  STRAIN-STERNE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         845 AA;
                                                                                                                                                                                                                                                                                                                                                                                      506
536
603
608
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                                                                                                                                    Glycoprotein.
INIT_MET
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CONFLICT
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MOD_RES
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. BIOL. Chem. 268:16679-16687(1993).

-1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
-1- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF AXONAL CALIBER.

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILLAMENT FUNCTION.
                           -----DATDAQVTVQNNSVITVGQGAKAGETYKVTVVLDGKLITTHSFKVVDTAPTA 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-92332596; Pubmed-1321159;
Kelly B.M., Gillespie C.S., Sherman D.L., Brophy P.J.;
"Schwann cells of the myelin-forming phenotype-express neurofilament
                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Glycosylation of mammalian neurofilaments. Localization of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93346421; PubMed-8344946;
Dong D.L.-Y., Xu Z.-S., Chevrier M.R., Cotter R.J., Cleveland D.W.,
Hart G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O-linked N-acetylglucosamine moieties on neurofilament polypeptides
 LL----
                                                                                                                                                                                                                                                                                                                                                                                                       rat NF-M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92165797; PubMed=1537832; Xu Z.-S., Liu W.-S., Willard M.B.; Identification of six phosphorylation sites in the COOH-terminal tail region of the rat neurofilament protein M."; J. Biol. Chem. 267:4467-4471(1992).
                                                                                                                                                                                      01-007-1989 (Rel. 12, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NF-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY
346 VDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYK--LVINGKTLKGET---
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87282618; PubMed-2441012; Napolitano E.W., Chin S.S.W., Colman D.R., Liem R.K.H.; "Complete amino acid sequence and in vitro expression of the middle molecular weight neurofilament protein."; J. Neurosci. 7:2590-2599(1987).
                                                                                                                                                                845 AA.
                                                          ----- NDNGVDGV 419
                                                                                     709 KGLAVEFTSTSLKEVAPNADLKAALLNILSVDGV 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION SITES, AND REVISION TO 500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Biol. 118:397-410(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYDRATE-LINKAGE SITES.
                                                                                                                                                                STANDARD;
                                                          KAVDAETAEKAFKOYA---
                                                                                                                                                                                                                                                                     NEF3 OR NEFM OR NFM.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  631 KVEEKKEVAKESPKEEKVEKKE--EKPKDVPDK-------KKAESPVKEKAVE-E 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 LIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EE-PKEEVTIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 TINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V------DVADKGYTLNIKFAGKEK----TPEEPKEEVTIKANLIYADGKTQTAEFK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QESKKEDIAINGEVEGKEEEEQETQEKGSGQE------EEKGVVTNGLD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VSPAEEKKGEDRSDDKVVV------TKKVEKITSE------GGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 676 MITITKSVKVSLEKDTKEEKPQQQEKVKE-KAEEEGGSEEEVGD-------KSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97;
                                                            InterPro; IPR001664; IF.
Pfam; PF00038; filament; 1.
PROSTIE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             502 PHOSPHORYLATION.
506 PHOSPHORYLATION.
536 PHOSPHORYLATION.
608 PHOSPHORYLATION.
666 PHOSPHORYLATION.
17 MISSING (IN REF. 2).
21 R -> P (IN REF. 2).
204 V -> L (IN REF. 2).
500 MISSING (IN REF. 1).
500 MISSING (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3%; Score 141.5; DB 1;
23.4%; Pred. No. 0.73;
ve 51; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                    /FIIG-CAR_000130.
0-LINED (GLCNAC).
/FIIG-CAR_000131.
PHOSPHORYLATION.
PHOSPHORYLATION.
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                               O-LINKED (GLCNAC)
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                                                                                                                                                                   BY SIMILARITY. HEAD.
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                                                                                                                                                                                                                                                                                                                LINKER 12
                                                                                                                                                                                                                                                                         LINKER 1.
                                                                                                                                                                                                                                                                                                                                        2A.
                                                                                                                                                                                                                                                                                               COIL 1B.
                                                                                                                                                                                                                                                                                                                                                                               COIL 2B.
                                                                                                                                                                                                                                                   COIL 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
EMBL; M18628; AAA41696.1; -. EMBL; Z12152; CAA78136.1; -. GlycoSuiteDB; P12839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 23.4%; es 92; Conservative 5
                                                                                                                                                                                                                                                                       147
246
263
285
285
410
47
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us-08-325-278b-3.rsp

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MEDLINE-97405699; PubMed-9260743;
MEDLINE-9740569; PubMed-9260743;
MEDLINE-9740569; PubMed-9260749;
MEDLINE-974099; PubMed-9260749;
MEDLINE-974099; PubMed-9260749;
MEDLINE-974099; PubMed-9260749; PubMed-92607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nerve levels are high early in development but decrease during postnatal development and are low in adults. In dorsal root gangila levels remain high throughout development. In dorsal root INDUCTION: By nerve growth factor.

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

PTM: LC1 is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by protecolytic processing. It is free to associate with of MAPIB (By similarity).
                        01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Microtubule-associated protein 18 (MAP 1B) (Neuraxin) [Contains: MAP1
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J., Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.; "Neuraxin, a novel putative structural protein of the rat central aervous system that is immunologically related to microtubule-associated protein 5."; EMBO J. 8:2879-2888(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAUTION: A C-terminal fragment of this protein (residues 1597 2459) was originally described as neuraxin in ref.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu D., Fischer I.; "Isolation and sequencing of the 5' end of the rat microtubule-associated protein (MAPIB)-encoding cDNA."; Gene 172:307-308(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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domains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain, and Glial tumor; MEDLINE-92347374; PubMed-1639092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zauner W., Kratz J., Staunton J., Feick P., Wiche G.
"Identification of two distinct microtubule binding
recombinant rat MAP 1B.";
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-142 FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-TESTIS;
MEDLINE-96257242; PubMed-8666295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3ur. J. Cell Biol. 57:66-74(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Spinal cord;
MEDLINE=90059871; Pubmed=2555150;
   O9ER21; Q9QW92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: TO MAP1A.
                                                                                                                                                                                                         Rattus norvegicus (Rat).
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                                                                                                                                               light chain LC1].
MAP1B.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1698 EEPSYTQDNDLSELISV--SQVEASPSTSSAHTPSQIASPLQE-----DTLSDVVPPRDM 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1751 SLYASLASEKVQSLE----GEKLSPKSDISPLTPRESSPTYSPGFSDSTSGAKESTAAYQ 1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1807 TSSSPPIDAAAAEPYGFRSSMLFDTMQHHLALSRDLTTSSVEKDNGGKTPGDFNYAYQKP 1866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIK-ANLIYADG------KTQTAEFK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 GT----FEEATAEAYRYAD-----ALKKDNGEYTVDVADKGYT---LNIKFAGK 153
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                                                                                                                                                                                                                                                                                                                                                                          CONTAINS MANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 NGKYTVDVADKGYTLNIKFAGKEKTPEEPKE-----EVTIKANLIYADGKTQTAEFKGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEK----PEEPMDTYKLIL
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between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW; 2E3F6872DEDB8BA2 CRC64;
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T -> S (IN REF. 1).
R -> K (IN REF. 3).
L -> I (IN REF. 3).
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                                                                or send an email to license@isb-sib.ch).
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GLU-RICH.
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MAPIB 3.
MAPIB 4.
MAPIB 5.
MAPIB 6.
MAPIB 6.
MAPIB 7.
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                                                                                                                                                                                          Phosphorylation
                                                                                                                                                InterPro; IPR000102; MAP1B_neuraxin.
                                                                                                                                                            Pfam; PF00414; MAP1B_neuraxin; 10.
PROSITE; PS00230; MAP1B_NEURAXIN; 8.
                                                                                                                      EMBL; X16623; CAA34620.1; ALT_SEQ.
PIR; S06017; S06017.
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Search completed: October 29, 2002, 09:30:03 Job time : 19.571 secs

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OM protein - protein search, using sw model

October 29, 2002, 09:27:36; Search time 18.2057 Seconds (without alignments) 2290.646 Million cell updates/sec Run on:

US-08-325-278B-3
2235
1 AVENKEETPETPETDSEEEV......GVDGVWTYDDATKTFTVTEM 434 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues

Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query	Query Match Length	DB	ID	Description
1	2235	100.0	455	5	A45063	immunoqlobulin-bin
7	1587.5	71.0	719	7	A42808	Ig light chain-bin
e	1263.5	56.5	992	7	S54396	protein L precurso
4	708	31.7	593	7	S00128	protein G precurso
5	706.5	31.6	664	7	S42574	
9	683	30.6	448	7	A24496	IgG-binding protei
7	404	18.1	413	7	855890	plasma protein rec
89	188.5	8.4	1185	7	A42404	collagen adhesin -
6	182	8.1	479	7	T47561	late embryogenesis
10	175	7.8	448	7	H84782	late embryogenesis
11	171.5	7.7	74	7	A34483	Iq liqht chain-bin
12	168	7.5	448	7	JC6171	late embryogenesis
13	162	7.2	913	7	T52485	neurofilament prot
14	159	7.1	1856	7	C95008	immunoglobulin Al
15	159	7.1	2551	7	B98047	hypothetical prote
16	157.5	7.0	1166	7	T28680	fibrinogen-binding
17	157	7.0	798	7	I50479	neurofilament medi
18	156.5	7.0	701	7	H98120	choline binding pr
19	156	7.0	916	7	A27864	
20	155	6.9	555	7	804909	embryonic protein
21	154.5	6.9	1110	7	151116	NF-180 - sea lampr
	154.5	6.9	1822	7	S33441	EF protein - Strep
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25		6.9	1873	7	T30944	surface protein pr
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30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 A45063 immunoglobulin-binding protein LG - Peptostreptococcus magnus c; species: Peptostreptococcus magnus C; Species: Peptostreptococcus magnus C; Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999 C; Accession: A45063 E; Abibergy B. M.; Sjobring, U; Kastern, W.; Bjorck, L. J. Biol. Chem. 267, 25583-25588, 1992 A; Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties. A; Reterence number: A45063; MUID:93094283 A; Status: preliminary A; Accession: A45063 A; Status: preliminary A; Ressidues: 1-455 < KIH> A; Kotessocial etypes mRNA; protein A; Cross-references: GB:S50809; NID:g261705; PIDN:AAA03280.1; PID:g261706 A; Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBIP:120303)	Gaps 0;	60 81	120 141	180 201	240 261	300 321	360 381	420
s nge 15-Oct bulin bind PID:92617 NCBIP:120	455;	AYADTLKKDN 	KGTFEEATAE KGTFEEATAE	IYADGKTQTA 	EPKEEVTIKA EPKEEVTIKA	NIRFAGKKVD 	TYDDATKTFT TYDDATKTFT	ANDNGVDGVW
RESULT 1 A45063 immunoglobulin-binding protein LG - Peptostreptococcus magnus C;Species: Peptostreptococcus magnus C;Species: Peptostreptococcus magnus C;Accession: A45063 C;Accession: A45063 R;Kihlberg, B.M.; Sjobring, 1932 R;Kihlberg, B.M.; Sjobring, 1932 A;Title: Protein LG: a hybrid molecule with unique immunoglobulin binding p A;Reference number: A45063; MUID:93094283 A;Accession: A45063 A;Accession: A45063 A;Status: preliminary A;Molecule type: mRNA; protein A;Residues: 1-455 cKIH> A;Residues: 1-455 cKIH> A;Residues: Begins CREINORD NID:9261706;A;Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBIP:120303)		AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN 	GEYTVDVADKGYTLNIKFACKEKTPEEPKEEVTIKANLIYADCKTQTAEFKGTFEBATAE 	AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 	EFKGTFEEATAEAYRYADELAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA 	NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 	EKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFT 	VTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVW 420
OStreptocc 8-Nov-1994 W.; Bjorc ith unique 13 O5; PIDN:A	Score 2235; DB 2; Pred. No. 1.9e-110; 0; Mismatches 0;	IGSTQTAEFKC IGSTQTAEFKC	EVTIKANLIY 	AGKEKTPEEP 	VADKGYTLNI)LLAKENGKYT 	ATAEKVFKQY ATAEKVFKQY	GETTTKAVDA
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RESULT 1 A45063 immunoglobulin-binding protein LG - C;Species: Peptostreptococcus magnus C;Accession: A45063 E;Accession: A45063 R;Kihlberg, B.M.; Sjobring, U.; Restlinger, C;Accession: A45063 A;Title: Protein LG: a hybrid molecu A;Reference number: A45063; MUID:930 A;Accession: A45063 A;Accession: A5063 A;Accession: A5063 A;Accession: A5063 A;Accession: A55063 A;Accession: A65063 A	Query Match Best Local Similarity 100. Matches 434; Conservative	AVENKEETPE 	GEYTVDVADK GEYTVDVADK	AYRYADALKK 	EFKGTFEEAT EFKGTFEEAT	NLIYADGKTQ NLIYADGKTQ	EKPEEPMDTY EKPEEPMDTY	VTEKPEVIDA
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           Ny Alternate names: protein L
C. Species: Peptostreptococcus magnus
C. Accession: Ava1094 * Resquence_revision 19-May-1994 * text_change 07-May-1999
C. Accession: Ava1080 * Ava1094 * Resquence_revision 19-May-1994 * text_change 07-May-1999
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C; Species: Peptostreptococcus magnus
A; Variation 3316
C; Date: 27-Oot-1996 #sequence_revision 13-Mar-1997 #text_change 15-Oct-1999
C; Accession: S54396
B; Murphy, J.P.; Duggleby, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDE 301
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395 KPEBKEQVTIKENIYFEDGTVQTATFKGTFABATA--RYADLLSKEHGKYTADLEDG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 TFTVT------EKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAE 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPEEPMD-TYK--LILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVD-GEWTYDDATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 light chain-binding protein precursor - Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.0%; Score 1587.5; DB 2; Length 719; 76.3%; Pred. No. 3.2e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 GYTINIRFAGKEEPEETPEKPEVOD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 KAFKQYANDNGVDGVWTY 422
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Matches 334; Conservative
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C; Species: Streptococcus sp.
A; Variety: Streptococcus sp.
A; Variety: Streptococcus sp.
A; Variety: Streptococcus sp.
A; Variety: Streptococcus sp.
C; Date: 30-Jun-1989 #text_change 19-May-2000
C; Accession: S00128; A27604; A26314
R; Olsson, A: Eliasson, M; Guss, B: Nilsson, B:; Hellman, U.; Lindberg, M.; Uhlen, Bir. J. Blochen. 168, 319-324, 1987
A; Title: Structure and evolution of the repetitive gene encoding streptococcal protein A; Reference number: S00128
A; Reference number: S00128
A; Reference number: S00128
A; Residues: 1-53 < OLS>
A; Residues: 1-53 < OLS
A; Reference number: A27604; MUID:88154455
A; Reference number: A27604
A; Molecule type: protein
A; Residues: 62-101 < SJOS
A; Residues: 62-101 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
Mol. Microbiol. 12, 911-920, 1994
A/Title: The functional units of a peptostreptococcal protein L.
A/Reference number: S54396; MUID:95020613
A/Accession: S54396
A/Status: preliminary; nucleic acid sequence not shown
A/Rolecule type: DNA
A/Residues: 1-992 < MURA
A/Residues: EMBL:L04466; NID:9150673; PIDN:AAA67503.1; PID:9150674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 MERKLSEKETPE--PEEEVTIKANLIFADGSTQNAEFKGTFAKAVSDAYAYADALKKDNG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | : | | : | | : | | : | | 657 EPGEDTPEVQEGYATYE------BAEABAKEALKEDKVNNAYEVVQGADGRYYY 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K-----VDE-----KPEEPM------DTY-KLILNGKTLKG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ET-----TTEAVDAATAEKVFKQYAND-----NGVDGEWTYDDATKTFTVTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 AEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein G precursor - Streptococcus sp. (Streptococcus G148)
N;Alternate names: albumin-binding protein; cell wall-bound protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.5%; Score 1263.5; DB 2; Length
58.8%; Pred. No. 4.9e-59;
Live 36; Mismatches 90; Indels
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A;Title: The type-III Fc receptor from Streptococcus dysgalactiae is also an alpha(2) A;Reference number: S42574; MUID:94192673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Fahnestock, S.R.; Alexander, P.; Nagle, J.; Filpula, D. J. Bacteriol. 167, 870-880, 1986
A; Fitle: Gene for an immunoglobulin-binding protein from a group.G Streptococcus. A; Reference number: A24496; MUID:86304178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A24496
A; Molecule type: DNA
A; Cross-references: GB: M13825; NID:g153822; PIDN: AAA03664.1; PID:g153823
A; Cross-references: GB: M13825; NID:g153822; PIDN: AAA03664.1; PID:g153823
A; Sicobring, U.; Bjoerck, L.; Kastern, W.
A; Title: Streptococcal protein G; Gene structure and protein binding properties.
A; Reference number: A39041; MUID:91093154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Streptococcus sp.
C.Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 17-Mar-2000
C.Accession: A24496; A39041
                                                                                                                                                                                                                                                                                                                                                                                                          ---GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVD 417
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                    A;Cross-references: EMBL:Z29666; NID:g470220; PIDN:CAA82764.1; PID:g470221
C;Superfamily: M5 protein
                                                                                                                                                                                                                                                                                            24 ANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK-KDNGEYTVDVADKGYTL--NIKFA- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 KGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 DEKPE--EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATK
                                                                                                                                                                                                     Length
                                                                                                                                                                                                  31.6%; Score 706.5; DB 2;
43.9%; Pred. No. 5.2e-30;
tive 51; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IgG-binding protein - Streptococcus sp. (group G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 34-42,'N',45-48;62-76;186-200 <SJO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVWTYDDATKTFTVTEM 434
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                     Best Local Similarity
Matches 192; Conserva
                                                                                         A; Molecule type: DNA
A; Residues: 1-664 <JON>
                                                                    A; Status: preliminary
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                                                A; Accession: S42574
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Best Local (
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C; Superfamily: M5 protein
C; Superfamily: M5 protein
E; H-33 Domain: signal sequence #status predicted <SIG>F: 34-593 /Porduct: protein G #status experimental <MAT>F: 34-116 /Domain: alanine-rich <ALA>F: 34-116 /Domain: alanine-rich <ALA>F: 34-116 /Pomain: Ab duplication <DUPI>F: 34-117-290 /Pomain: A repeat
F: 341-191 /Region: A repeat
F: 341-391 /Region: A repeat
F: 361-393 /Pomain: IgG binding <IGB>F: 363-397 /Region: C repeat
F: 358-372 /Region: C repeat
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-May-2000
C;Accession: S4257 # Nueller, H.P.
Eur. J. Biochem. 220, 819-826, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 YTVDVADKGYTLNIK-FAGKEKTPEE----PKEEVTIKANLIYADGKTQTAEFKGTFAE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A--TAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE-------EPMDTY 310
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    ю
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KTQTAEFKGTFEEATAEAYRYADALKKDNGE---YTVDVADKGYTLNIKFAGKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 LSDFLKSQTP-----AEDTVKSIELAEAKVLANRELDKYGVSDYHKNLINNAKTVEGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 TPEEPKEEVTIKANLIYA-DG-----KTQTAEFKGTFEEATAEAYRYAD---LLAKENGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFT
                                                                    A;Molecule type: DNA
A;Residues: 114-593 <GUS>
A;Cross-references: GB:X04015; NID:g47071; PIDN:CAA27638.1; PID:g47072
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.7%; Score 708; DB 2; Length 59:
48.3%; Pred. No. 3.7e-30;
iive 28; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               streptococcal surface protein - Streptococcus dysgalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;443-497/Region: C repeat
F;498-567/Domain: proline-rich <PRO>
F;568-593/Domain: carboxyl-terminal <CTD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205; Conservative
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VTEM 498
                                             A; Accession: A26314
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Best Local S
Matches 205
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gen adhesin - Staphylococcus aureus
ccies: Staphylococcus aureus
ccies: Staphylococcus aureus
cci 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995
cession: A42404; S27665
ti, J.M.; Jonsson, H.; Guss, B.; Switalski, L.M.; Wiberg, K.; Lindberg, M.; Hook
Li, J.M.; Jonsson, H.; Guss, B.; Switalski, L.M.; Wiberg, K.; Lindberg, M.; Hook
Lie: Molecular characterization and expression of a gene encoding a Staphylococcu
erence number: A42404; MUID:92165839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 RY-ADALKKDNGEYT-VDVADKG-----YT----LNIKFAGKEKTPEEPKEEVTIKA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853 INESNNWTHTWTGLDEKAKGQQVKYTVEELTKVKG-YTTHVDNNDMGNLIVTNKYTPETT 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 --AGKKV-DEK-----PEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 GVDGEWTYDDATK-TFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     630 TVTKNWDDNNNQDGKRPTEIKVEL-YQDGKATGKTAILNESNNWTHTWTGLDEKAKGQQV 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 -----TAEFKGTFAEATAEAYRY-ADLLAKENGKYTADLED---GGYTINIRF---- 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 SEA---YAYADTLKKDNG-------EYTVDVADKGYTLNIKFAGKEKTPEEPKE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IKANLIYADGKTQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLIYADG-KTQTAEFKGTFEEATAEA---YRYADLLAKENGK------YTVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ry Match 8.4%; Score 188.5; DB 2; Length 1185; t Local Similarity 23.8%; Pred. No. 0.016; ches 136; Conservative 61; Mismatches 166; Indels 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s: sequence extracted from NCBI backbone (NCBIP:83982)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 ADKGYTLNIKFAGKEKTPEEPKEEVT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tus: preliminary
ecule type: DNA
idues: 1-1185 <PAT>
ss-references: EMBL:M81736
                                                                                                      tents: FDA 574
ession: A42404
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C; Species: Peptostreptococcus magnus
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-1996
C; Dates 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-1996
C; Accession: A34483
R; Akerstroem, B: Bjoerck, L.
J. Biol. Chem. 264, 19740-19746, 1989
A; Title: Protein L: an immunoglobulin light chain-binding bacterial protein. Characte
A; Reference number: A34483; MUID:90062074
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A;Molecule type: DNA
A;Residues: 1-448 <STO>
A;Residues: 1-448 <STO>
A;Cross-references: GB:AE002093; NID:g4415909; PIDN:AAD20140.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g36640
A;Map position: 2
                                                                                                                                                                                                                                                                                        79 EAAESTKEGAQIASEKAVGAK-------DATVEKAKET----ADYTAEKVGE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 KGTFEEATAE------AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---EPKEEV--TIKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLED 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 GGYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAAT----AEKV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 --FKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASEL------TPAVTTYKL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 VGEYKDYTVDKAVEARDYTAEKAIEAKDKTAEKTGEY-----KDYTVEKATEGKDVTVS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 EETKDSAAVRGNEAKGTIFGALGNVTEAIKSKLTMPSDIVEETRAAREHGGTGRTVVEVK 407
                                                                                                                                                                                                                                                    3 ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGE 62
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                                                                                                                                                                                                                                                                                                                                                                     259 KLGELKDSAVETAKRAMGFLSGKTEEAKGKAVETKDT------AKE-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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                                                                                                                                                             DB 2; Length 448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 VINGKTLKGETTTKAVDAETAEKAFKQYANDNG-VDGVWTYDDATK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 171.5; DB 2;
Pred. No. 0.0042;
                                                                                                                                                        7.8%; Score 175; DB 2; L 24.5%; Pred. No. 0.025; tive 50; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 EKTPEEPKEEVTIKANLIYADGKTQTAEFKG-----
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58.2%;
                                                                                                                                                                                Best Local Similarity 24.5%
Matches 114; Conservative
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A;Molecule type: protein
A;Residues: 1-74 <AKE>
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                             Query Match
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (Mouse-ear cress)
C; Accession: H84782
R; Lin, X; Kaul, S; Rounsley, S.D; Shea, T.P; Benito, M.I; Town, C.D; Fujli, C.Y; M; Koo, H; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. ebis, D; Neture 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487
A; Status: preliminary
                                     late embryogenesis abundant protein-like - Arabidopsis thaliana
N;Alternate names: protein F8J2.210
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47561
R;Nyakatura, G:; Fartmann, B:; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 DNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 DTAESTREGADIASEKAAGMR-----DTTGEVRDSTAQKTKETADYTADKAREAKD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 EEPKEEV-TIKANLIYADGKTQ----TAEFKGTFAEATAEAYRYADLLAKENGKYTADL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 EDGGYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 NGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDA--- 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAY----ADTLKK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AEAYRYA-DALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 QTAEFKGTFEEATAE-----AYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.1%; Score 182; DB 2; Length 47 ilarity 24.1%; Pred. No. 0.012; Conservative 59; Mismatches 195; Indels
                                                                                                                                                                       Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A.Reference number: Z24458
A.Accession: T47561
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-479 < CNYA>
A.Cross-references: EMBL.AL132969
A.Experimental source: cultivar Columbia; BAC clone F8J2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ETAEKAFKQYANDNGVDGVWTYDDATK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPGYVATVLKEADQMTGQTFNDVG-----EIDDEEK 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 110; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 3
A;Introns: 329/3; 382/2
A;Note: F8J2.210
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RESULT 9
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Query Match 7.2%; Score 162; DB 2; Length 913;	tromosome 4. 9y 51 AYADTLKKDNGEYTUDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKT	Qy 225 KEKTPEEPKEEVTIKANLIVADGKTQTAEFKGTFA EATAEAYRYADLLAKE NGKY	119 Db 713 122 QY 322 165 Db 770	YTAEF 182 Qy 378 TTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDA 425	RESULT 14 C95008 immunoglobulin Al proteinase [imported] - Streptococcus pneumon: C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change C;Accession: C95008 347 R;Tettellin, H; Nelson, K.E.; Paulsen, J.A.; Read,	"TYKL 382 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001 A.Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916 A.Actatus: preliminary	- African clawed frog -Oct-2000	Query Match e molecular weight neu Best Local Similarity 23.1%; Score 159; DB 2; Length 1856; Best Local Similarity 23.1%; Pred. No. 1; Matches 119; Conservative 60; Mismatches 176; Indels 160; Gaps 28; Qy 7 ETPETPETDSEEEVTIKANL-IFANGSTQTAEFKGTFEKAT-SEAYAYAD 54
c6171 ate embryogenesis abundant protein - Arabidopsis thaliana ate embryogenesis embryogenic cell protein 63: phosphotyrosine pri Species: Arabidopsis thaliana (mouse-ear cress) Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 21 Accession: JG6171 Accession: JG6171 Saitou, T.; Komeda, Y.; Harada, H.; Kamada, H.	Gene 184, 83-88, 1997 A,Title: Arabidopsis thaliana ECP63 encoding a LEA protein is located in change and the protein is located in change Economic strates and the protein is located in change Economic strates and the protein is located in change at the protein Expansion: JC6171 A; Molecule type: mRNA A; Molecule type: mRNA A; Rossidues: 1-448 < YAN> A; Cross-references: DBBJ:D64140; NID:g1526423; PIDN:BAA11017.1; PID:g152642 C; Comment: This protein is a phosphotyrosine protein which belongs to late C; Genetics: A; Genetics: A; Genetics: A; South part C; Kewwords: seed	tch al Similarity 24.2%; Score 168; DB 2; Length 448; al Similarity 24.2%; Pred. No. 0.059; 113; Conservative 50; Mismatches 161; Indels 142; G ENKEPTPETDESERYTKANLIFANGSTQTAEFKGTFEKATSEAYANDTLKKDNGE	79 EAAESTKEGAQIASEKAVGAKDATVEKAKETADYTAEKVGE 63 YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGFFEEATAEAY 1	123 RYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEF 1 1 1 1 1 1 1 1 1 1	231EPKEEVTIKANLIYADGKTQTAEFKGTFABATAEAYRYADLLAKENGKYTADLED 259 KLGELKDSAVETAKRAMGFLSGKTEEAKGKAVETKDTAKE 286 GGYTINIRFAGKKVDEKPEEPMDTYKLILNGKTLKGETTTEAVDATAEKV	337FKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKL :	tein NF-M(2), middle molecular weight [imported] s laevis (African clawed frog) 00 #sequence_revision 24-Oct-2000 #text_change 24	Nietrasi, C.; Szalo, B.G. Brain Res. Mol. Brain Res. 48, 229-242, 1997 A;Title: Sequence and expression pattern of two forms of the middle A;Teference number: 226090 A;Steference number: 226090 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residnes: 1-013, GCRA

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C;Species: Streptococcus pneumoniae
C;Accession: B98047
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E.
R; Hoskins, J.A.; Alborn Jr., W.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N.
Y, P.; Sun, P.M.; Winkler, M.E.
J; Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B98047
A;Accession: B98047
A;Accession: preliminary
A;Accession: Lype: DNA
A;Residues: 1-2551 KURP>
A;Cross-references: GB:AE007317; PIDN:AAL00207.1; PID:g15459054; GSPDB:GN00174
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430 NIPYTTEEIQDPTLLKNRRKIERQG---QAGTRTIQYEDYIVNGNVVETKEVSRTEVAPV 486
                                                                                                                                                              143 GYTLNIKFAGKEK-----TPEEPKEEVTIKANLI----YADGKTQTAEFKGTFEEA 189
                                                                                                                                                                                                                                                        190 TAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEP-KEEV-----TI 238
                                                                                                                                                                                                                                                                                        239 KANLIYADG------KTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTIN 291
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                                                                                                                                                                                              166 IKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGK
                                                                      ---TAEFKGTFEEATAEAYRYADALKKDNGEYT-----VDVADK
                                                                                                                                                                                                                                                                                                                                                                                | :| | | | :| :| : : : | | | | :| : | 569 KTHLTYNLGENNEENTETSTQDFQLEXKKIEIKDIDSVELYGKENDRY------
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23.0%; Pred. No. 1.5;
tive 46; Mismatches 162; Indels 150;
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Matches 107; Conservative
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Search completed: October 29, 2002, 09:31:33 Job time : 24.2057 secs

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
 MOLECULE TYPE: protein
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STATE: Washington
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784.805 Million cell updates/sec
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                                                                                                            ; Search time 13.5074 Seconds
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             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-485-286-19
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Maximum Match 100%
Listing first 45 summaries
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Sequence Sequence

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ö Gaps AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN 60 Sequence 12, Sequence 38, Sequence 38, Sequence 38, Sequence 10, Sequence 10, Sequence 6, Sequence 6, Sequence 68, Sequenc Sequence Sequence Sequence Sequence ; 0 Length 434; APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14 CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,475
FILING DATE: 11-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTers, David D.
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
FELECOMMUNICATION NUMBER: 100084.40201
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-631
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids ORIGINAL SOURCE: ORGANISM: Escherichia coli LE392/PHDLG, DSM 7055 100.0%; Score 2235; DB 2; ilarity 100.0%; Pred. No. 1.8e-170; Conservative 0; Mismatches 0; ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue US-08-446-137B-5 US-09-117-233-16 US-09-117-233-12 US-09-117-233-12 US-09-117-2926-38 US-09-117-233-10 US-09-117-233-10 US-09-117-233-10 US-09-117-233-6 US-09-117-233-6 US-09-058-459-44 US-09-058-459-58 US-09-058-459-70 US-09-058-459-68 US-09-127-926-68 US-09-058-459-46 US-09-058-459-43 ALIGNMENTS MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 3, Application US/08795475 Patent No. 5965390 GENERAL INFORMATION: õ

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MOLECULE TYPE: protein
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                             61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE
                                                                                        AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bjvrck, Lars
APPLICANT: Sjvbring, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli LE392/pHDL, DSM 7054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/795,475
FILING DATE: 11-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTERTS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.4021
TELECOMMNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08795475 Patent No. 5965390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                        421 TYDDATKTFTVTEM 434
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                                           Gaps
                                                                                                                                                                           61 GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120
                                                                                                                                                                                                                                                                 121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180
                                                                                                           1 AVENKEETPETPETDSEEEVTIKANLIFANGSTOTAEFKGTFEKATSEAYAYADTLKKDN 60
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Patent No. 6162903
GENERAL INFORMATION:
APPLICANT: Trowern, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Laurence, Oliver S.
APPLICANT: Laurence, Oliver S.
APPLICANT: Laurence, Oliver S.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
TITLE OF INVENTION: PROM L PROTEIN AND THEIR USES
NUMBER OF SEQUENCES: 12
Length 305;
                                           Indels
  Score 1565; DB 2; I
Pred. No. 2.6e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
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                                             Mismatches
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REFERENCE/DOCKET NUMBER: 100084.406
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JANEER: US/08/446,137B
22-MAY-1995
           100.08; Pr
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: McMasters, David D. REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS: LENGTH: 1027 amino acids
  70.0%;
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                                             Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: SEED and
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Washington
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Query Match
Best Local Similarity
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301 EKPEE 305
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60 KGLTLNIKFAGKKEKPEEPKEEVTIKVNLIFADGKTQTAEFKGTFEEATAKAYAYADLLA 119
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                                                                                                                                                                                                                                                                                                                                                                                                             130 KDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFE 187
                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                             10 ETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: JONSSON, Hans
APPLICANT: LINDBERG, Martin
APPLICANT: MUELER, Hans-Peter
APPLICANT: MATHAMAKI, Liisa K.
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING
TITLE OF INVENTION: PLASMAPROTEINASE INHIBITOR-BINDING PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,408B
                                                                                                                                                                                      DB 4;
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                                                                                                                                                                                    ; Score 1216; D; Pred. No. 1.6e 20; Mismatches
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APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9302855-3
FILING DATE: 06-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 2000/->12.COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
~~weither: IBM PC compatible
~~weither: IBM PC compatible
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   (206) 622-4900
                                                                                                                                                                                      54.4%;
82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-1996
                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
                                                                                                                                                                                    Query Match 54.49
Best Local Similarity 82.59
Matches 241; Conservative
                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LA
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                                                                                            TYPE: amino acid
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US-08-669-408B-2
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                                                                                                                                                                                  EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                          Gaps
                                                                                                             61
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                                        Length 1027;
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APPLICANT: Laurence, Oliver S.
APPLICANT: Laurence, Oliver S.
APPLICANT: Duggleby, Clive J.
TITLE OF INVENTION: IMMUNGELOBULIN BINDING PROTEINS DERIVED
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                    56.5%; Score 1263.5; DB 4; Length
58.8%; Pred. No. 1.5e-92;
.ive 36; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MOMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Trowern, Angus R. APPLICANT: Atkinson, Anthony
                                                                        Conservative
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MEDIUM TYPE: Floppy
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STATE: Washington
                                    Query Match
Best Local Similarity
Matches 281; Conserv
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US-08-446-137B-2
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TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : : | | : | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 FAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 DAGFNSQHGVTLTVT-OGK----QVQKWDRISKAAFEWADHPTAVIPDMQKLGIKDKNEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 ---KPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 502;
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 27.9%; Score 622.5; DB 1; Best Local Similarity 41.1%; Pred. No. 6.3e-42; Matches 178; Conservative 36; Mismatches 136;
            26-JAN-1995
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Patent No. 5646026
Patent No. 5646026 5646119
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFRENCE/DOCKET NUMBER: 3827;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: ANDREA T. BORUCKI
9330 ZIONSVILLE ROAD
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APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acid
TYPE: amino acid
                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) MOLECULE TYPE: protein US-08-378-761A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 TYDDATKTFTVTE 433
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CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                     FILING DATE: 26 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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Patent NO. 5635384
GENERAL INFORMATION:
PAPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 ANEIVINSDAYTAESIQPLYKLINDAY---DVLESKDYSKY--DSQDKVNNLADQLRDAV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 ------GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 DALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 KGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 DEKPE--EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 ANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK-KDNGEYTVDVADKGYTL--NIKFA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 QAVQLEAPTVIDAPELTPALTTYKLVVKGNTF--SGETTTK----AIDTATAEKEFKQYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 GNTF--SGETTTKAIDAATAEKEFKQYATANGV---DGEWSYDDATKTFTVTEKPA---V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 TFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKOYANDNGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                Query Match 31.6%; Score 706.5; DB 3; Best Local Similarity 43.9%; Pred. No. 1.9e-48; Matches 192; Conservative 51; Mismatches 143;
61743/102
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9330 ZIONSVILLE ROAD
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IBM PC compatible
                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                               TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                    : 664 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           543 GVWTYDDATKTFTVTEM 559
                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
OPERATING SYSTEM: PC
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CORRESPONDENCE ADDRESS:
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CITY: INDIANAPOLIS
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US-08-378-761A-25
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RIBOSOME-INACTIVATING PROTEINS, INACTIVE
PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
USING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 TVSRTVDAGFNSQHGVTLTVTQGKQVQKWDRISKAAFEWADHPTAVIPDMQKLGIKDKNE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE-----EPMDTYKLILNGKTL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTY 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKPEVIDASELTPAVTTYKLVINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTY 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEV---TIKANLIYADG---- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTE-----
                                                                                                                                                                                                                                                                                                                                   COMPUTER REDDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KTQTAEFKG------TFAEATAEAYRYAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.8%; Score 622; DB 1;
46.9%; Pred. No. 6.7e-42;
tive 28; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/08485286
Patent No. 5646026
Patent No. 5646026 5646119
                                                                                                                   STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (317) 337-4846 INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WALSH, TERENCE A
HEY, TIMOTHY D
MORGAN, ALICE ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 3365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.9%
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-378-761A-23
                                                                                                                         CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: RITILE OF INVENTION: PHITLE OF INVENTION: US NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDATKTFTVTE 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: WALSH, TAPPLICANT: HEY, TINAPPLICANT: MORGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                            46268
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                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 EEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADALKKDNGEYTVDVADKGYTLNIK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 FAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 DAGFNSQHGVTLTVT-QGK----QVQKWDRISKAAFEWADHPTAVIPDMQKLGIKDKNEA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 YRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE------EPMDTYKLILNGK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVW 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 EFKGTF-----EKATSEAYAYADTLKKDNGEYTVDV-ADKGYTLNIKFAGKEKTPEEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 DLAKKKKAADPQ-----SDTKSKLVK----LVVMVCEGLRFNTV----SRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 DHKGIFQPVLPPEKKVPELWFYTE-LKTRTSSITLAIRMDNLYLVGFRTPG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.9%; Score 622.5; DB 1; Length 41.1%; Pred. No. 6.3e-42; ive 36; Mismatches 136; Indels
                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
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33651
38272B
                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILLING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (317) 337-4846 INFORMATION FOR SEQ ID NO: 25:
                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502 amino acids
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                                                         COMPUTER READABLE FORM:
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                                                                                   MEDIUM TYPE:
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US-08-378-761A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF TITLE OF INVENTION: PRODUCING SAME NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza STATE: According Carden City Plaza STATE: NA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Trailinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 KATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKESAWRHPQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
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Pred. No. 8.4e-42;
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                                                                                                                                                                                                                        New York : United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGBNT INPORMATION:
NAME: DIGIGIOL Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/POCKET NUMBER: 100
TELECOMMUNICATION INFORMATION:
TELEFAN: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFAX: (516) 742-4366
TELERX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
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75.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS: LENGTH: 342 amino acids
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                                                                                                                                                                                                                                                                 ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: New York
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Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                           COUNTRY:
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STATE:
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                                    PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF USING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 TVSRTVDAGFNSQHGVTLTVTQGKQVQKWDRISKAAFEWADHPTAVIPDMQKLGIKDKNE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 ---LLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE------EPMDTYKLILNGKTL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AARIVALVKNOTTAAAATAG-SVNV-----DKPEVIDASELTPAVTTYKLVINGKTL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 - KPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKOYANDNGVDGVWTY 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 SKPEVIDASELTPAVTTYKLVINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTY 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 KGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTE-------
              RIBOSOME-INACTIVATING PROTEINS, INACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 ---KTQTAEFKG-------TFAEATAEAYRYAD-----
                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Datem: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.8%; Score 622; DB 1;
Best Local Similarity 46.9%; Pred. No. 6.7e-42;
Matches 146; Conservative 28; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 38272B TELECOMMUNICATION INFORMATION:
TITLE OF INVENTION: RIBOSOME-INACTITLE OF INVENTION: PRECURSOR FOI TITLE OF INVENTION: USING NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: ANDREA T. BORUCKI STREET: 9330 ZIONSVILLE ROAD CITY: INDIANAPOLIS STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANY: Koentgen, Frank
APPLICANY: Suess, Gabriele M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (317) 337-4846 INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: 493 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-485-286-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDATKTFTVTE 433
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                           ZIP: 46268
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United States of America

ZIP: 11530

COUNTRY:

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RIBOSOME-INACTIVATING PROTEINS, INACTIVE
PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
USING
                                                                                                                                                                                                                                                                                                          16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 -----GVWWEFGKDGDTHLLGDNPRWLGFGGRYQD-LIGNKGLETVTMGRAEMTRAVN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 PEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDD 424
                                                                                                                                                                                                                                                                                                                                              37 EFKGTF-----EKATSEAYAYADTLKKDNGEYTVDV-ADKGYTLNIKFAGKEKTPEEPK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 FACKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 DLAKKKKAADPQ-----SADTKSKLVK----LVVMVCEGLRFNTV----SRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 DV---ADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQT-AEFKGTFAEATAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 DAGFNSQHGVTLTVT-QGK----QVQKWDRISKAAFEWADHPTAVIPDMQKLGIKDKNEA
                                                                                                                                                                                                                                                                                                                                                                      266 YRYADLLAKENGKYTADLEDGGYTINIRFAGKK---VDEKPEEP-MDTYKLILNGKTLKG
                                                                                                                                                                                                                                                                     27.7%; Score 618; DB 1; Length 489; 40.8%; Pred. No. 1.4e-41;
                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                          35; Mismatches 131;
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Patent No. 5646026
Patent No. 5646026 5646119 ·
                 NAME: BORUCKI, ANDREA T
REGISTRATION UNUMBER: 3851
REFERENCE/DOCKET UNMBER: 3827
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: ANDREA T. BORUCKI
9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-I
TITLE OF INVENTION: PRECURSOR
TITLE OF INVENTION: USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       489 amino acids
                                                                                                                                                                                                                                                                                         Best Local Similarity 40.83
Matches 175; Conservative
                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-378-761A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T.
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                                                                                                                                                                           amino acid
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                                                                                                                                                       LENGTH:
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APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: USING
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA I. BORUCKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PKEEVTIKANLIYADGKTQTAEFKGTFE 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 SEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 EATAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
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ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

""TWARE: PatentIn Release #1.0, Version #1.25
""C'08/378,761A
                                             SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 8.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.7%; Score 618; 75.9%; Pred. No. 8
                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: DiG19110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPRIS: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/08378761A Patent No. 5635384 GENERAL INFORMATION:
                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: ANDREA T. BORUCKI
9330 ZIONSVILLE ROAD
                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          342 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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PatentIn Release #1.0, Version #1.30
                           E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                  United States of America
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELES: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 178 amino acids
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      CORRESPONDENCE ADDRESS:
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                                         STREET: 400 CTTY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11530
                                                                                                             COUNTRY: UN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GVWWEFGKDGDTHLLGDNPRWLGFGGRYQD-LIGNKGLETVTMGRAEMTRAVN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 FAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEAYRYADLLAKENGKYTV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 EFKGTF-----EKATSEAYAYADTLKKDNGEYTVDV-ADKGYTLNIKFAGKEKTPEEPK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 DV----ADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQT-AEFKGTFAEATAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 ARIVALVKNQT-----TAAAATAGSKPEVIDASELTPAVTTYKLVINGKTLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 PEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 DHKGIFOPVLPPEKKVPELWFYTE-LKTRTSSITLAIRMDNLYLVGFRTPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Roentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlain, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.7%; Score 618; DB 1; Length 48
40.8%; Pred. No. 1.4e-41;
Live 35; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTE-----
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDRER: 33651
REFERENCE/COCKET UNMBER: 33672B
TELECOMMUNICATION INVORMATION:
TELECOMMUNICATION INVORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 19:
                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
                                                                                                                                                                                                                                                                                                                                                                                                       489 amino acids
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-485-286-19
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Best Local Similarity
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US-08-828-741B-13
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78 FAGKEKTPEE---------PKEEVTIKANLIYADGKTQTAEFKGTFEEA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.5%; Score 615; DB 3; Length 178; 76.2%; Pred. No. 5.9e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09160567
Patent No. 6326179
GENERAL INFORMATION:
APPLICANT: Suess, Gabriele M.
APPLICANT: Tariliton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 TAEAYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPK 161
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/828,741B
FILING DATE: 26-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MURPHY & PRESSER
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Pred. No. 5.9e-42;
5; Mismatches 14; Indels ;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGALIO, FRAN S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELEPHONE: (516) 742-443
TELEPHONE: (516) 742-436
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 27.5%;
Best Local Similarity 76.2%;
Matches 125; Conservative
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Search completed: October 29, 2002, 09:31:57 Job time : 16.5074 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

October 29, 2002, 09:25:06 ; Search time 34.0622 Seconds (without alignments) 1415.233 Million cell updates/sec Run on:

US-08-325-278B-3
2235
1 AVENKEETPETPETDSEEEV......GVDGVWTYDDATKTFTVTEM 434 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

747574 seqs, 111073796 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence encoding	Immunoglobulin lig	Amino acid sequenc	Expression vector	Protein L. Peptoc	Protein L. Peptoc	Immunoglobulin bin	S. dysgalactiae MI	Streptococcus Prot	Streptococcus GX78	Sequence of polype
		ΩI	AAR42994	AAR42993	AAB31372	AAB10432	AAR42203	AAR43699	AAR42204	AAR71929	AAR62944	AAR10005	AAP70468
		DB:	14	14	22	21	14	14	14	16	15	12	œ
		Match Length DB ID	434	305	467	367	1027	1027	291	664	593	594	480
ф	Query	Match	100.0	70.0	69.4	61.4	56.5	56.5	54.4	31.6	31.4	31.4	31.0
		Score	2235	1565	1550	1372	1263.5	1263.5	1216	706.5	702	701.5	692.5
	Result	. ON .	-	7	3	4	2	9	7	8	6	• 10	11

Protein G variant Protein G. Strept Protein G. Strept	. 8	Streptococcus Prot	IgG-binding Strept	Type 4 GX7809 prot	IgG-binding Strept	Streptococcus stra	G	G		Protein G variant.	Type 3 GX7809 prot	IgG-binding Strept	Protein G variant.	Protein G variant.	Type 9 GX7809 prot	IgG-binding Strept	Protein G variant.	Protein G variant.	Type 2 GX7809 prot	IgG-binding Strept	Type 8 GX7809 prot	IgG-binding Strept	Protein G variant.	Protein G variant.	Type 1 GX7809 prot		Protein G variant.	Protein G variant.	Protein G variant.	Protein G variant.
AAR07014 AAP70493 AAP95030	AAR07013	AAR53290	AAR53295	AAR10011	AAR53294	AAY57610	AAP94785	AAR07004	AAP94784	AAR07003	AAR10009	AAR53293	AAP94787	AAR07011	AAR10015	AAR53299	AAP94783	AAR07002	AAR10007	AAR53292	AAR10013	AAR53298	AAP94782	AAR07001	AAR10008	AAR53291	AAR07010	AAP94788	AAR07006	AAP94790
11	112	12	15	12	12	21	10	11	10	11	12	15	10	11	12	15	10	11	12	15	12	15	10	11	12	15	11	10	11	10
593 448	448	* *	269	265	265	185	235	235	144	144	144	144	164	164	164	164	199	199	199	199	201	201	148	148	148	148	201	569	569	201
31.0												29.7			29.7				29.7		29.7	29.7	29.4	29.4	29.4	29.4	29.4		29.0	28.9
692 683 683	683	683	675	674	674	670	999	665	663	663	663	663	663	663	663	663	663	663	663	663	663	663	658	658	658	658	657	959	648	646
133	15	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAR42994 standard; Protein; 434 AA. (6-MAY-1994)(first entry) AAR42994 AAR4 2994

Sequence encoding immunoglobulin light chain binding protein.

Immunoglobulin; light chain; binding; identification; purification; separation; ss.

E. coli L392/pHDLG, DSM 7055.

/label= B1 immunoglobulin light chain binding domain. /label= B2 immunoglobulin light chain binding Location/Qualifiers 81..305 Domain Domain

/label- B3 immunoglobulin light chain binding /label= B4 immunoglobulin light chain binding domain. domain. 153..305 297..305 225..305 от вшос Ооmain Jomain

domain.

/label= B5 immunoglobulin light chain binding domain.

Domain

309..434 /label= C1 immunoglobulin heavy chain binding

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421 TYDDATKTFTVTEM 434
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                                                                                                                  16-MAY-1994
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                                                                                                                                                                            separation
                                                                                            AAR42993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKPEEPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVW 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New protein L binding light chains of all immunoglobulin classes - for binding purifying and identifying immunoglobulin, also related DNA, vectors and host cells
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                                            /label= C2 immunoglobulin heavy chain binding
364..434
/label- D intermediate immunoglobulin heavy
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                        chain binding domain.
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100.0%;
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Matches 434; Conservative
                                 379..434
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                                                                                                                                                                                                                       WPI; 1993-368722/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                            434 AA;
                                                                                                                                                                                                                                    P-PSDB; AAR42994
                                                                                                                            28-APR-1993;
                                                                                                                                                   28-APR-1992;
                                                                               WO9322342-A.
                                                                                                      11-NOV-1993
                                                                                                                                                                                                 Bjoerck L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
  Domain
                                  Domain
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The protein (Protein L) is capable of binding to immunoglobulin G light chains. It is useful for binding, separating (purifying) and identifying immunoglobulin and for removing immunoglobulin molecules from serum. Hybrid proteins of the L protein can bind all human immunoglobulin classes and many immunoglobulins from other species. They are highly soluble and retain their binding activity at high victoratures over a pH range of 3-10. They can be immobilised without loss of activity.
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                                                                                                                                                                                                                            Immunoglobulin; light chain; binding; identification; purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New protein L binding light chains of all immunoglobulin classes - for binding purifying and identifying immunoglobulin, also related DNA, vectors and host cells
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/label= Bl immunoglobulin light chain binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin light chain binding
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                                                                                                                                                                     Immunoglobulin light chain binding protein (Protein L).
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Pred. No. 1.4e-84;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 36; 71pp; English.
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100.0%; Pr
tive 0;
AAR42993 standard; Protein; 305
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Best Local Similarity 100.
Matches 305, Conservative
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N-PSDB; AAQ50452.
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N-PSDB; AAA71428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a method for expressing and isolating are excembinant protein in a plant. The method comprising expressing a fusion protein including the recombinant protein and a cellulose binding peptide fused to it, where the fusion protein is compartmentalised and sequestered within plant cells, plant derived tissue or cultured plant cells. The method is useful for obtaining large quantities of the recombinant proteins and protein products in a simple and cost-effective manner. Recombinant proteins may be used commercially, such as in the food processing industry, e.g. glucoamylases and glucose isomerases are used for converting starch to high fructose corn syrup, proteinases for the hydrolysis of high molecular weight proteins and in
                                                                                    240
                                120
                                          121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180
                                                                                                                                                              NLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVD 300
                                                                                                                                                                         Protein production; food processing; protein antibiotic; feed enzyme; protein L: CBD cex protein; cell signal peptide.
                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of protein L/CBD cex/ER retaining peptide fusion.
           9
                                                                                                                               Expressing and isolating recombinant protein in a plant, useful for producing large quantities of recombinant proteins, by expressing fusion protein including a cellulose binding peptide fused to a recombinant protein.
GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE
                                                                                                                    EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TECHNOLOGIES LTD.
SUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                  AAB31372 standard; Protein; 467 AA.
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(YISS ) YISSUM RES DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shani Z, Shoseyov O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-112219/12.
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                                                                                                                                                                                                         EKPEE 305
                                                                                                                                                                                                                            EKPEE 305
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manufacturing leather or alcoholic beverages, pectinesterases for pectin hydrolysis in food industry, lipses for cleaving ester linkage in triglycerides, and for effluent treatment. The recombinant proteins may further be used to produce protein antibiotics, which can be used in healing processes, and to produce animal feed enzymes. The present sequence represents a fusion protein of the invention, and comprises a fusion of a cell signal peptide, protein L, CBD cex, and an endoplasmic reticulum retaining peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AYRYADALKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEKPEEPMDTYKLILNGKTLKGETTTEAVDAA------TAEKVFKQYANDN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 DEKPEGIPPT-----PTPTSASGPAGCQVLWGVNQWNTGFTAQVTVKN-TGSA 386
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      1 AVENKEETPETPETDSEEEVTIKANLIFANGSTOTAEFKGTFEKATSEAYAYADTLKKDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 AVENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYEYADTLKKDN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFKGTFEEATAEAYRYADLL-AKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIK
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                                                                                                                                                                                                                                                                                                                                                                   40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVDG-WTL----TFSFPSGQQVTQAWSSTVTQSGSAVTVRNAPWNGNIPAGGT 434
                                                                                                                                                                                                                                                                                                         Length 467;
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                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                         Score 1550; DB 2;
Pred. No. 1.8e-83
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression vector pSEX11L4 protein G.
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                                                                                                                                                                                                                                                                                                            69.48;
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                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 328; Conserv
                                                                                                                                                                                                                                                      467 AA;
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wall binding.
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                                                                                                                                                                                                                                                             W09322439-A
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                                                                                                                                                                                                                                                                                                                                                                                                  antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies cells to produce antibody-producing hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The combination of the signal peptide of a murine immunoglobulin (Ig) Kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule; an antibody-binding site of proteins A, G, L or LG, and the transmembrane domain of PDEFK (platelet-derived growth factor receptor) or CDS2. The method is used to select MAb with specificity for particular antigens. MAb can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in MAb selection. This sequence represents the protein G, Neo-R and the bla protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for the selection of monoclonal
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                                            Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.4%; Score 1372; DB 21; Length 367; 82.4%; Pred. No. 3.6e-73; ive 19; Mismatches 29; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 EPMDTYKLILNGKTLKGETTTEAVDAATA 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 1027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunoglobulin binding proteins derived from Protein {\tt L} -which bind immunoglobulin kappa light chains but not albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1263.5; DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                     Trowern AR;
/label= Signal sequence.
60..968
/label= Mature protein L.
                                                                                                                                                                                                                                                                                                                                                    (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD
                                                                                                                                                                                                                                                                                                                                                                                                   Murphy JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Figure 1; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.5%;
58.8%;
                                                                                                                                                                                                                   93WO-GB00950
                                                                                                                                                                                                                                                                    92GB-0009804
92GB-0026928
                                                                                                                                                                                                                                                                                                                                                                                                     CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Duggleby
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-368798/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1027 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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K-----KPEEPM-
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                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                        WPI; 1993-368798/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 AA;
                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ50947
                                ----ET---
                                                                                                                                                        18-MAY-1994
                                                                                                                                                                                                                                                                07-MAY-1993;
                                                                                                                                                                                                                                                                                 07-MAY-1992;
                                                                                                                                                                                                                                                                                        24-DEC-1992;
                                                                                                                                                                                                                                                                                                                         Atkinson A,
                                                                                                                                                                                                                                 WO9322439-A.
                                                                                                                                                                                                                                                11-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 241;
                                                                                                                                                                                                                 Synthetic.
                                                                                                                                        AAR42204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK
                                                                                                                                                                                                                                                                                                                                               Protein L forms a complex with immunoglobulin Kappa light chain. Purified protein can be used as a reagent for immobilising antibodies e.g. on columns, in diagnostic tests and in assays. may also be used in the production of pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 1027
                                                                                                                                                                                                                                                                                                 used for prodn.
                                                                               Protein; immunoglobulin; binding; immobilisation; light chains;
                                                                                                                                                                                                                                                                                                                                                                                                                         90; Indels
                                                                                                                                                                                                                                                                                              Immunoglobulin binding polypeptide, protein L - used for of pharmaceuticals and for immobilising antibodies e.g. columns, in diagnostic tests and in assays
                                                                                                                                                                                                                                                         Trowern AR;
                                                                                                                                                                                                                                                                                                                                                                                                       56.5%; Score 1263.5; DB 58.8%; Pred. No. 2.7e-66; ive 36; Mismatches 90
                                                                                        antibodies; diagnosis; pharmaceutical; ss
                                                                                                                                                        ij
                                                                                                                               36..59
/label= Signal sequence.
60..968
/label= Mature protein I
                                                                                                                                                                                                                                       (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
                                                                                                                                                                                                                                                         Murphy JP,
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                                                                                                                       Location/Qualifiers
               AAR43699 standard; Protein; 1027
                                                                                                                                                                                                                                                                                                                              Claim 4; Figure 1; 29pp; English.
                                                                                                                                                                                                        93WO-GB00949
                                                                                                                                                                                                                       92GB-0009804
                                                (first entry)
                                                                                                                                                                                                                                                         Duggleby CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                       WPI; 1993-368797/46.
P-PSDB; AAR43699.
                                                                                                                                                                                                                                                                                                                                                                                       1027 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 281; Conserv
                                                                                                        magnus
                                                                                                                                                                                                        07-MAY-1993;
                                                                                                                                                                                                                       07-MAY-1992;
                                                                                                       Peptococcus
                                               18-MAY-1994
                                                                                                                                                                      WO9322438-A.
                                                                                                                                                                                                                                                        Atkinson A,
                                                                                                                                                                                       11-NOV-1993
                                                                Protein L.
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                               AAR43699;
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                                                                                                                               Peptide
                                                                                                                                               Protein
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Matches
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                                                                                                                        Key
        AAR43699
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574 EQPGENPGITIDEWLLKNAKEEAIKELKEAGITSDLYFSLINKAKTVEGVEALKNEILKA 633
                                                                                                                          -TTEAVDAATAEKVFKQYAND-----NGVDGEWTYDDATKTFTVTEK 364
.-- 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The synthetic immunoglobulin binding proteins derived from protein L comprise repeated sequences from protein L which bind immunoglobulin kappa light chains. They can be used in protein analysis, purification procedures and other biochemical processes e. g. ELISA. The synthetic molecules are of particular advantage if they are free of regions in protein L which exhibit albumin and cell wall binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVAD 69
                                                                                                                                                                                                                                                     365 PEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTY 422
                                                                                                                                                                                                                                                                                             EPGEDTPEVQEGYATYE------EAEAAAKEALKEDKVNNAYEVVQGADGRYYY 739
                                                                                                                                                               Peptide; immunoglobulin; binding; analysis; purification; ELISA; enzyme linked immunoabsorbant assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunoglobulin binding proteins derived from Protein {\bf L} -which bind immunoglobulin kappa light chains but not albumin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
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-----DTY-KLILNGKTLKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin binding protein derived from protein L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trowern AR;
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82.5%; Pred. No. 3.9e-64;
iive 20; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR42204 standard; Protein; 291 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Figure 2; 28pp; English.
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obtain prods. for sepn., detection or quantification or for
 to obtain prods. for binding inhibition
                                                                                                                                                                                                    664 AA;
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                    EATAEAYRYADILLAKENGKYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYA 245
                                                                                          KDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQTAEFKGTFE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding fast alpha 2-macro:globulin-binding proteins - used
                                                                                                                                               DGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rantamaki LK;
                                                                                                                                                              /note= "putative wall anchoring motif" 639..664
                                                                                                                                                                                                                                                                                                                                                                                                                    fast alpha-2-macroglobulin binding protein; FAM; na proteinase-inhibitor binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "cell wall spanning region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "membrane spanning domain"
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/label= IgG1
/note= "IgG binding domain 1"
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279..348
/label= IgG2
'~~te= "IgG binding domain 2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mueller H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= IgG3
/note= "IgG binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= IgG4
/note= "IgG binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= IgG5
/note= "IgG binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus dysgalactiae strain SC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..30
/label=_Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                            A.
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                                                                                                                                                                                                                                                                      AAR71929 standard; Protein; 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-SE00826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANTAMAKI L K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jonsson H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-123382/16.
N-PSDB; AAQ89196.
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LINDBERG M.
MUELLER H.
                                                                                                                                                                                                                                                                                                                                                                                    S. dysgalactiae MIG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                22-SEP-1995
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(LIND/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                         plasma
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130
                                   120
                                                                     188
                                                                                                       180
                                                                                                                                           246
                                                                                                                                                                               240
                                                                                                                                                                                                                                                       AAR71929
                                                                                                                                                                                                                                        RESULT
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analyzed
                                                                                                                                                                                                                                                                                                                                                                           203 QAVQLEAPTVIDAPELTPALTTYKLVVKGNTF--SGETTTK----AIDTATAEKEFKQYA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 TANNVD-GEWSYDDATKTFTVTEKPAVIDAPELTPALTTYKLIVKGNTF--SGETTT--- 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482
                                                                                                                                                                                                                                                                                               ------GKEKTPEEPKEEVTIKANLIYADGKTQTAEFKGTFEEATAEA--YRYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                             DALKKDNGEYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIKANLIYADGKTQTAEF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 DEKPE--EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATK 357
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 ANLIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 ANLIFANGSTQTAEFKGTFEKATSEAYAYADTLK-KDNGEYTVDVADKGYTL--NIKFA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 KGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFA---GKEKTPEEPKEEVTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 GNTF--SGETTTKAIDAATAEKEFKQYATANGV---DGEWSYDDATKTFTVTEKPA---V
                                                                                                                                                                                                                               51;
                                                                                                                                                                                           Length 664;
                                 A phage lambda GEM-11 library of S. dysgalactiae SCI DNA was a for fast-acting alpha-2-macroglobulin (FAM)- and IgG-binding activity. One clone, which expressed both activities, was analyzed to obtain DNA encoding the FAM-binding protein, MIG (AAR71929). The mig gene is given in AA089196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor
                                                                                                                                                                                       ; Score 706.5; DB 16; Length; Pred. No. 7.4e-34; 51; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus Protein G derived from strain GX7805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= al
/note= "linking region"
179..215
/label= A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593
                                                                                                                                                                                           31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR62944 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106..140
/label= A1
141..178
50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                         Query Match
Best Local Similarity 43.99
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVWTYDDATKTFTVTEM 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus sp. GX7805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 GVWTYDDATKTFTVTEM
Disclosure; Page 31;
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Gaps

90;

Length 593; Indels 370

434

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160 LSDFLKSQTP-----AEDTVKSIELAEAKVLANRELDKYQVSDYHKNLINNAKTVEGVK 213
                                                                                                                                                                     207 YTVDVADKGYTLNIK-FAGKEKTPEE-----PKEEVTIKANLIYADGKTQTAEFKGTFAE 260
                                                     -----KTQTAEFKGTFEEATAEAYRYADALKKDNGE---YTVDVADKGYTLNIKFAGKEK 155
                                                                                                                                                                                                               261 A--TAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE------EPMDTY 310
                                         45 ATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYA-DG 103
                                                                                                                                               214 DLQAQVVESAKKARISEATDGLSDFLKSQTP----AEDTVKSIELAEAKVLANRELDK
                                                                                                                                                                                                                           268 YGVSDYYKNLINNAKTVEGVKALIDEILAALPKTD-TYK---LILNGKTLKGE---TTTE
                                                                                                                                                                                                                                                       KLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDA
                                                                                                                            156 TPEEPKEEVTIKANLIYA-DG----KTQTAEFKGTFEEATAEAYRYAD---LLAKENGK
                    28; Mismatches 132;
  31.4%; Score 702; DB 15;
48.1%; Pred. No. 1.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374..428
/label= Active Site B3
444..498
/label= Active Site B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304..358
/label= Active Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus GX7805 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
88US-0209236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-0354264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0354264
Query Match 31.4%
Best Local Similarity 48.1%
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus sp GX7805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emmunoglobulins; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                     1111
495 VTEM 498
                                                                                                                                                                                                                                                                                                                                        431 VTEM 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1986;
17-FEB-1987;
19-JUN-1987;
20-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US4977247-A
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                                                                                                                                                                                                                                                                                                                                                                                                              AAR10005
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR10005;
                                                                                                                                                                                                                                                       311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A 2.4kb HindIII fragment containing the entire coding sequence for Protein G was isolated from Streptococcus GX7805 using the 1.9kb Protein G coding sequence from Streptococcus GX7809. The Frotein G has IgG-binding activity which has been localised to the B repeating structure. Streptococcal Protein G variants comprising the B domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant streptococcal protein G variants - useful for antibody detection and purification and for therapy
                                                                      303..357
Alabel- Bl
force= "involved in 1gG binding activity"
358..372
                                                                                                                                                                                                                                          'note= "involved in IgG binding activity"
                                                                                                                                   373.427
/label= B3
/note= "involved in IgG binding activity"
                                                                                                                                                                                                                                                                                                                                                                                          /note= "corresponds to GAA codon"
                                                                                                                                                                             'note= "corresponds to CCT codon"
                                                             'note= "corresponds to GGA codon"
                                                                                                                                                                                                                                                               /note= "corresponds to ACT codon"
         /label= a2
/note= "linking region"
254..290
                                                                                                              /label b
/note "linking region"
                                                                                                                                                                                                           /note= "linking region"
443..497
/label= B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PHAA ) PHARMACIA LKB BIOTECHNOLOGY AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Fig 9; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          860S-0829354.
860S-0854887.
870S-0063959.
880S-0209236.
900S-0540169.
                                                                                                                                                                                                                                                                         531..535
/label= C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        86US-0829354
                                                                                                                                                                                                                                                                                           536..540
/label= C2
                                                                                                                                                                                                                                                                                                                 541..545
/label- C3
                                                                                                                                                                                                                                                                                                                                      546..550
/label= C4
                                                                                                                                                                                                                                                                                                                                                           551..555
/label= C5
                                        label= A3
                                                                                                                                                                                        428..442
/label- b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-159179/19.
N-PSDB; AAQ75036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                   Misc-difference
                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-1986;
23-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-1988;
19-JUN-1990;
                                                                                                                                     Active-site
                                                                                                                                                                                                                      Active-site
                                                                                                                                                                                                                                                                                                                                                                                                              US5312901-A
                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are claimed
                                                                        Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                  Region
 Region
                              Domain
                                                                                                        Region
                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                               Region
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KTPEEPKE-----EVTIKANLIYA-DG----KTQTAEFKGTFEEATAEAYRYADALKK 130
                                                                                                                                                                                                                                                          A recombinant DNA molecule containing a nucleotide sequence which codes for a protein or polypeptide having the same igG specificity protein G from Streptococcus G148 (AAN70757) is claimed. See, for example, AAN70754, AAN70754, AAN70755 and AAN70756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNGE---YTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYA-DG-----KTQTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AEDTVKSIELAEAKVLANRELDKYGVSDYYKNLINNAKTVEGVKALIDEILAALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTEAVDAATAEKVFKQYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 KTVEGVKDLQAQVVESAKKARISEATDGLSDFLKSQTP----AEDTVKSIELAEAKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 ANRELDKYGVSDYHKNLINNAKTVEGVKDLQAQVVESAKKARISEATDGLSDFLKSQTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 FKGTFEEATAEAYRYAD---LLAKENGKYTVDVADKGYTLNIK-FAGKEKTPEE----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEEVTIKANLIYADGKTQTAEFKGTFAEA - - TAEAYRYADLLAKENGKYTADLEDGGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIRFAGKKVDEKPE-----EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAET
                                                                                                                                                                                 New recombinant DNA molecules - for producing proteins with IgG-binding specificity of protein G or proteins A and G
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                  Score 692.5; DB 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEKAFKQYANDNGVDGVWTYDDATKTFTVTEM 434
                                                                                                       Uhlen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus sp. Lancefield Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä
                                                                                                       Flock JI,
                                                                                                                                                                                                                                                                                                                                                                 31.0%; Sco
49.7%; Pre
tive 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       593
                                                                                                                                                                                                                               Example; Fig 2; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein G variant with three
87WO-SE00145
                              86SE-0001325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Matches 195; Conservative
                                                                                                       BM, Lindberg KM,
                                                            (PHAA ) PHARMACIA AB
                                                                                                                                WPI; 1987-277686/39.
N-PSDB; AAN70757.
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR07014 standard;
                                                                                                                                                                                                                                                                                                                                    480 AA;
                                                                          (GUSS/) GUSS B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin.
20-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-1991
                              21-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR07014;
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403
                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                          Guss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132
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AAR0701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
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                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435
                                                                                                                                                                                                                                                                                                                      ATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYA-DG 103
                                                                                                                                                                                                                                                                                                                                         155
                                                                                                                                                                                                                                                                                                                                                                                                               213
                                                                                                                                                                                                                                                                                                                                                                                                                                             206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495
                                                                                                                                                                 Protein G gene product may be modified allowing the variant to
be imobilised and exhibit different binding profiles. The bound
protein is useful in purification and detection of Igs and fragments.
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 ----KTQTAEFKGTFEEATAEAYRYADALKKDNGE---YTVDVADKGYTLNIKFAGKEK
                                                                                                                                                                                                                                                                                                                                                                                                               160 LSDFLKSQTP-----AEDTVKSIELAEAKVLANRELDKYGVSDYHKNLINNAKTVEGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                           156 TPEEPKEEVTIKANLIYA-DG-----KTQTAEFKGTFEEATAEAYRYAD---LLAKENGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTVDVADKGYTLNIK-FAGKEKTPEE----PKEEVTIKANLIYADGKTQTAEFKGTFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 A--TAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE-----EPMDTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFT
                                                                                                                                                                                                                                                                                        59;
                                                                                        Immobilised protein G variants - used for detection, isolation and purificn. immunoglobulin(s) and immunoglobulin fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity
                                                                                                                                                                                                                                                          31.4%; Score 701.5; DB 12; ilarity 47.9%; Pred. No. 1.3e-33; Conservative 28; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of polypeptide possessing IgG-binding protein G from Streptococcus G148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody-binding; IgG; IgA; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP70468 standard; Protein; 480 AA.
               Wroble MH;
                                                                                                                                   Disclosure; Fig 9; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
              Lee T,
                                          WPI; 1991-006758/01
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 203; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus G148
                                                                                                                                                                                                                             594 AA;
                                                            Q-PSDB; Q10002
               Fahnestoc SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||
VTEM 499
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322

268 207

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376

436

431

496

70468 RESULT

17;

Gaps

65;

Length Indels

8;

186

181

342

402 353

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protein G expressed by inserting the gene into an expression vector. A second vector may also be used as a cryptic helper plasmid to stably maintain the first plasmid in the host call. Bacterial Fc receptors such as Protein G can be used to detect and purify antibodies, and in the treatment of disease. Fc receptors are useful to purify antibodies to be used in the purificn. of protein drugs and as therapeutics. High levels of Frotein G can be obtd. in conditions favourable for isolation, using a non-pathogenic host. Suitable cloning vectors are lambda gtll, M13mp9 and pGX1066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 KDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD-GKTQTAEFKGTFEE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 AAWEAAAAADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGIKDLQAQVVESAKKAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 RNGGELT------NLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 ATAEAYRYADLLA-----KENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIYA-DG-----KTQTAEFKGTFAEATAEAYRYAD---LLAKENGKYTADLEDGGYTINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloned Protein G gene – used for producing Protein G for detection and purificn. of antibodies and treatment of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.6%; Score 683; DB 8; Length 448; 53.2%; Pred, No. 1.1e-32; tive 15; Mismatches 92; Indels
                                                                                                                                                                                                                      Streptococcus Lancefield Group G strain.
                                                                                                                                                                                                                                                               228..297
/label=active site B1
298..352
/label=active site B2
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig. 3; 68pp; English.
                                                                                                                                                                                           Protein G; antibody; Fc receptor;
                                                                                AAP70493 standard; protein; 448
                                                                                                                                                                                                                                                                                                                                                                                        87WO-US00329
                                                                                                                                                                                                                                                                                                                                                                                                                    86US-0854997
                                                                                                                                                                                                                                                                                                                                                                                                                                  86US-0829354
                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.R.
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N-PSDB; AAN70811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 176; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAHN/) FAHNESTOCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENE-) GENEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 AA;
            495 VTEM 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ahnestock S;
                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-1986;
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                                                                                                                                                                                                                                                                                          Active-site
                                                                                                                                                                                                                                                                Active-site
                                                                                                                                                                                                                                                                                                                                                                27-AUG-1987
                                                                                                                                      06-MAR-1991
                                                                                                                                                                 Protein G.
                                                                                                            AAP70493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                      RESULT 13
                                                                   AAP70493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KTQTAEFKGTFEEATAEAYRYADALKKDNGE---YTVDVADKGYTLNIKFAGKEK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 A--TAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDEKPE------EPMDTY 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 LSDFLKSQTP----AEDTVKSIELAEAKVLANRELDKYGVSDYHKNLINNAKTVEGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPEEPKEEVTIKANLIYA-DG----KTQTAEFKGTFEEATAEAYRYAD---LLAKENGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 DLQAQVVESAKKARISEATDGLSDFLKSQTP-----AEDTVKSIELAEAKVLANRELDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTVDVADKGYTLNIK-FAGKEKTPEE----PKEEVTIKANLIYADGKTQTAEFKGTFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 KLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPEVIDA
                                                                                                                                                                                                                                                                                                                                                                                                                               Fragments and variants of the sequence are claimed esp. where incorporated into a non-pathogenic host eg. E.coli, and expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 593;
                                                                                                                                                                                                                                                                                                                                                              encoding Protein G from Streptococcus sp., used for binding
                                                                                                                                                                                                                                                                                                                                                 Recombinant Protein G variants - obtd. using a cloned gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.0%; Score 692; DB 11; Length 59 47.9%; Pred. No. 4.6e-33; ive 28; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 9; 48pp; English.
                                                                                                                                                             88US-0209236.
86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
                                                                                                                                    88US-0209236
            373..427
/label=B3
443..497
/label=B2
/label=B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 47.9 Matches 203; Conservative
                                                                                                                                                                                                                                                                                                    WPI; 1990-297491/39.
                                                                                                                                                                                                                                                  GENE-) GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 AA;
                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ06019
                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             high levels.
                                                                                                                                                                                                                                                                            Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 VTEM 434
                                                                                                                                    20-JUN-1988;
                                                                                                                                                                                                                      19-JUN-1987;
              Active-site
                                      Active-site
                                                                               US4956296-A
                                                                                                          11-SEP-1990
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                                                                                                                                                                                          23-APR-1986
17-FEB-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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203 INNAKTVEGVKELIDEILAALPKTDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragments and variants of the sequence are claimed esp. where incorporated into a non-pathogenic host eg. E.coli, and expressed at high levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The variants have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.6%; Score 683; DB 11; Length 448; 53.2%; Pred. No. 1.1e-32; Live 15; Mismatches 92; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding
                                                                                                                                                                                                                                                                                                                                           Streptococcus sp. Lancefield Group G strain.
                                                                                       EKAFKQYANDNGVDGVWTYDDATKTFTVTEM 434
                                                                                                       Protein G variant with two active sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 8a-c; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                               A
                                                                                                                                                                                            AAR07013 standard; protein; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86US-0829354.
86US-0854887.
87WO-US00329.
87US-0063959.
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/label=B1
298..352
/label=B2
                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolating antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-297491/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 176; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ06018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin.
                                                                                                                                                                                                                                                                                                               Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENEX
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23-APR-1986;
17-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-1988;
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Matches
                              344
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6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein G of non-pathogenic streptococcus and variants may be isolated, useful as bacterial Fc receptors eg in purification and detection of Abs. screening of hybridoma clones and treatment of disease.
                                293 RFAGKKUDEKPE------EPMDTYKLILNGKTLKGETTTEAUDAATAEKUFKQXAND 343
               --EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 343
                                                                        NGVDGEWTYDDATKTFTVTEKPEVIDASELTPAVTTYKLVINGKTLKGETTTKAVDAETA 403
                                                                                         130 KDNGEYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKANLIYAD-GKTQTAEFKGTFEE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 ATAEAYRYADLLA-----KENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 AAWEAAAAADALAKAKADALKEFNKYGVSDYYKNLINNAKTVEGIKDLQAQVVESAKKAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 RNGGELT------NLLGNSETTLALRNEESATADLTAAAVADTVAAAAAENAGA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 LIYA-DG-----KTQTAEFKGTFAEATAEAYRYAD----LLAKENGKYTADLEDGGYTINI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressing proteins having immunoglobulin-binding properties protein G and derived from Streptococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.6%; Score 683; DB 10; Best Local Similarity 53.2%; Pred. No. 1.1e-32; Matches 176; Conservative 15; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                            ds.
                                                                                                                                                EKAFKQYANDNGVDGVWTYDDATKTFTVTEM 434
                                                                                                                                                                                                                                                                                                                                                         immunoglobulin; Fc receptor;
                                                                                                                                                                                                                                     AAP95030 standard; protein; 448 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein G variant genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; ; 116pp; English.
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                                                                                                                                                                                                                                                                                                 (first entry)
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N-PSDB; AAN91093.
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             293 RFAGKKVDEKPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 AA;
                                                                                                                                                                                                                                                                                                                                                                                         sp.
                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-1988;
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                                                                                                                                                                                                                                                                                                                                                         Protein G;
                                                                                                                                                                                                                                                                                                                            Protein G.
                                                                                                                                                                                                                                                                 AAP95030;
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                                                                                                                                                             323
                                                                                                  263
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                                                                                                                                                                                                         RESULT 14
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242 LIYA-DG-----KTQTAEFKGTFAEATAEAYRYAD----LLAKENGKYTADLEDGGYTINI 292
                                            293 RFAGKKVDEKPE------EPMDTYKLILNGKTLKGETTTEAVDAATAEKVFKQYAND 343
                                                                               189 ATAEAYRYADLLA-----KENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN 241
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091c00 staphylococ
056193 staphylococ
056192 staphylococ
09rqt5 streptococc
09rqt5 streptococc
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017464 caenorhabdi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus sp.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-29094283; PubMed-1460053;
Kihlberg B.M., Sjobring U., Kastern W., Bjorck L.;
Protein LG: a hybrid molecule with unique immunoglobulin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 455;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, La
01-DEC-2001 (TrEMBLrel. 19, La
PROTEIN LG (FRAGMENT).
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Q53975 streptococc
Q54181 streptococc
Q56212 streptococc
Q5337 streptococc
Q5337 streptococc
Q5488 mandua sex
Q94888 mandua sex
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09skp0 arabidopsis
09s4k2 lactobacill
093ty6 staphylococ
096246 arabidopsis
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               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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sp_rodent:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murphy J.P., Trowern A.R., Duggleby C.J.,
"Nucleotide sequence of the gene for peptostreptococcal protein L.",
DNA Seq. 4.259-265(1994).
EMBL, LO4466, AAA67503.1; -.
HSSP: Q51911; 1GAB.
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                                                                                                   FKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKAN
                                                                                                                                      242 LIYADGKTQTAEFKGTFAEATAEAYRYADLLAKENGKYTADLEDGGYTINIRFAGKKVDE
                                                                                                                                                   KPEEPMD-TYK = - LILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVD-GEWTYDDATK
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108700 MW; 9CFF5771578A5DCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN L PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.5%; Score 1263.5; DB 2;
58.8%; Pred. No. 1.8e-53;
tive 36; Mismatches 90;
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Pfam; PF00746; Gram_pos_anchor; 1.
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MEDLINE-95078460; PubMed-7987012;
                                                                                                                                                                                                                                                                                         405 KAFKQYANDNGVDGVWTY 422
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Best Local Similarity 58.8
Matches 281; Conservative
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InterPro; IPR002988; GA.
InterPro; IPR001899; Gra
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992 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE-90215984; PubMed=2108927;
Kastern W., Holst E., Nielsen E., Sjobring U., Bjorck L.;
"Protein L, a bacterial immunoglobulin-binding protein and possible virulence determinant.";
Infect. Immun. 58:1217-1222(1990).
                                                        181 EFKGTFEEATAEAYRYADLLAKENGKYTVDVADKGYTLNIKFAGKEKTPEEPKEEVTIKA
                                                                                                                                                                         Peptostreptococcus magnus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Finegoldia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-312;

BJDLINE-9216971; PubMed-1618782;

BJOERCK L., Sjoebbing U., Kastern W.;

Structure of peptostreptococcal protein L and identification of repeated immunoglobulin light chain-binding domain.";

J. Biol. Chem. 267:12820-12825(1992).

EMBL. M86697; AAA256121.

EnterPro: IPR001899; Gram_pos_anchor.

Ffan: PF02246: B1; S.

Pfam: PF00246; Gram_pos_anchor.
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Q53291 streptococc
Q51912 peptostrept
Q53975 streptococc
Q9168 arabidopsis
Q93em8 streptococc
Q9skp0 arabidopsis
Q96246 arabidopsis
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Q91255 petromyzon
Q954k2 lactobacill
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ALIGNMENTS

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"Structure of peptostreptococcal protein L and identification repeated immunoglobulin 11ght chain-binding domain.";
J. Biol. Chem. 267:12820-12825(1992).
EMBL, M86697; AAA25612.1; ...
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InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF02246; B1; 5.
Pfam; PF00746; Gram_pos_anchor; 1.
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Bacteria; Firmicutes; Bacillus/Clostridium
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                                     KVDEKPEE 305
                                                                  YRYADALKKDNGEYTVDVADKGYTLNIKFAGKE--KTPEEPKEEVTIKANLIYADGKTQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Pred. No. 8.5e
22; Mismatches
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PROTEIN L.
9CFF5771578A5DCE CRC64;
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3.5e-60;
hes 31;
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